



SEQUENCE LISTING

<110> Hitoshi, Yasumichi
Jenkins, Yonchu
Markovtsov, Vadim
Rigel Pharmaceuticals, Inc.

<120> Modulators of Cellular Proliferation

<130> 021044-004010US

<140> US 10/620,052
<141> 2003-07-14

<150> US 60/395,443
<151> 2002-07-12

<160> 78

<170> PatentIn Ver. 2.1

<210> 1
<211> 2164
<212> DNA
<213> Homo sapiens

<220>
<223> protein kinase C, zeta (PKC-zeta), atypical
protein kinase C isoform

<400> 1
atgcccagca ggaccgaccc caagatggaa gggagcggcg gccgcgtccg cctcaaggcg 60
cattacgggg gggacatctt catcaccagc gtggacgccc ccacgacctt cgaggagctc 120
tgtgaggaag tgagagacat gtgtcgctcg caccagcagc acccgtcac cctcaagtgg 180
gtggacagcg aaggtgaccc ttgcacggtg tcctcccaga tggagctgga agaggctttc 240
cgccctggccc gtcagtgcag ggtatgaaggc ctcatcatc atgttttccc gagcacccct 300
gagcagcctg gcctgcccattc tccgggagaa gacaatcta tctaccgccc gggagccaga 360
agatggagga agctgtaccg tgccaaacggc caccctttcc aagccaagcg cttaacagg 420
agagcgtact gcggtcagtg cagcgagagg atatggggcc tcgcgaggca aggctacagg 480
tgcataact gcaaaactgct ggtccataag cgctgcccacg gcctcgcccc gctgacactgc 540
aggaagcata tggattctgt catgccttcc caagagcctc cagtagacga caagaaccgag 600
gacgcccacc ttccttccga ggagacagat ggaattgctt acatttccctc atcccgaaag 660
catgacagca ttaaagacga ctggaggac cttaagccag ttatcgatgg gatggatgga 720
atcaaaatct ctcaggggct tgggctgcag gactttgacc taatcagagt catggggcgc 780
gggagctacg ccaaggttct cctggtgcgg ttgaagaaga atgaccaaatttacgcatg 840
aaagtggta agaaaagagct ggtgcatgt gacgaggata ttgactgggt acagacagag 900
aagcacgtgt ttgagcaggc atccagcaac cccttcctgg tcggattaca ctccctgcttc 960
cagacgacaa gtcgggtgtt cctggtcatt gagtacgtca acggcgggga cctgatgttc 1020
cacatgcaga ggcagaggaa gctccctgag gacgacgcca gttctacgc ggccgagatc 1080
tgcatacgccc tcaacttcct gcacgagagg gggatcatct acagggacatc gaagctggac 1140
aacgtcctcc tggatgcgga cgggcacatc aagtcacag actacggcat gtgcaaggaa 1200
ggcctggccc ctgggtgacac aacgagact ttctgcggaa ccccgaattt catgcccccc 1260
gaaatcctgc ggggagaggaa gtacgggttc agcgtggact ggtggcgct gggagtcctc 1320
atgtttgaga tggatggccgg ggcgtccccg ttgcacatca tcaccgacaa cccggacatg 1380
aacacagagg actacctttt ccaagtgtatc ctggagaagc ccattccggat ccccccgggttc 1440
ctgtccgtca aagcctccca tggatggatggatggatggatggatggatggatggatggatgg 1500
ctcggtgcgc ggccacagac tggatggatggatggatggatggatggatggatggatggatgg 1560
atagactggg acttgctgga gaagaagcag ggcgtccctc cattccagcc acagatcaca 1620
gacgactacg gtctggacaa ctttgacaca cagttcacca ggcggccgt gcaagctgacc 1680
ccagacgatg aggtatgcatt aaagaggatc gaccatgtca agttcgaagg ctttgagttat 1740
atcaacccat tattgctgtc caccgaggag tcggatgttag ggcgtcgct tctctgtcgt 1800

ggacacgcgt gattgaccct ttaactgtat ccttaaccac cgcatatgca tgccaggctg 1860
ggcacggctc cgagggcgcc cagggacaga cgcttgcgcc gagaccgcag agggaaagcgt 1920
cagcgggcgc tgctgggagc agaacagtcc ctcacacctg gcccggcagg cagttcgtg 1980
ctggaggaac ttgctgctgt gcctgcgtcg cggcgatcc gcggggaccc tgccgagggg 2040
gctgtcatgc gtttccaag gtgcacattt tccacggaaa cagaactcga tgcactgacc 2100
tgctccgcca ggaaagttag cgttagcgt cctgaggaat aaaatgttcc gatgaaaaaa 2160
aaaaa 2164

<210> 2
<211> 592
<212> PRT
<213> Homo sapiens

<220>
<223> protein kinase C, zeta (PKC-zeta), atypical
protein kinase C isoform

<400> 2
Met Pro Ser Arg Thr Asp Pro Lys Met Glu Gly Ser Gly Gly Arg Val
1 5 10 15

Arg Leu Lys Ala His Tyr Gly Gly Asp Ile Phe Ile Thr Ser Val Asp
20 25 30

Ala Ala Thr Thr Phe Glu Glu Leu Cys Glu Glu Val Arg Asp Met Cys
35 40 45

Arg Leu His Gln Gln His Pro Leu Thr Leu Lys Trp Val Asp Ser Glu
50 55 60

Gly Asp Pro Cys Thr Val Ser Ser Gln Met Glu Leu Glu Glu Ala Phe
65 70 75 80

Arg Leu Ala Arg Gln Cys Arg Asp Glu Gly Leu Ile Ile His Val Phe
85 90 95

Pro Ser Thr Pro Glu Gln Pro Gly Leu Pro Cys Pro Gly Glu Asp Lys
100 105 110

Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu Tyr Arg Ala
115 120 125

Asn Gly His Leu Phe Gln Ala Lys Arg Phe Asn Arg Arg Ala Tyr Cys
130 135 140

Gly Gln Cys Ser Glu Arg Ile Trp Gly Leu Ala Arg Gln Gly Tyr Arg
145 150 155 160

Cys Ile Asn Cys Lys Leu Leu Val His Lys Arg Cys His Gly Leu Val
165 170 175

Pro Leu Thr Cys Arg Lys His Met Asp Ser Val Met Pro Ser Gln Glu
180 185 190

Pro Pro Val Asp Asp Lys Asn Glu Asp Ala Asp Leu Pro Ser Glu Glu
195 200 205

Thr Asp Gly Ile Ala Tyr Ile Ser Ser Ser Arg Lys His Asp Ser Ile
210 215 220

Lys Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Met Asp Gly
 225 230 235 240

Ile Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg
 245 250 255

Val Ile Gly Arg Gly Thr Tyr Ala Lys Val Leu Leu Val Arg Leu Lys
 260 265 270

Lys Asn Asp Gln Ile Tyr Ala Met Lys Val Val Lys Lys Glu Leu Val
 275 280 285

His Asp Asp Glu Asp Ile Asp Trp Val Gln Thr Glu Lys His Val Phe
 290 295 300

Glu Gln Ala Ser Ser Asn Pro Phe Leu Val Gly Leu His Ser Cys Phe
 305 310 315 320

Gln Thr Thr Ser Arg Leu Phe Leu Val Ile Glu Tyr Val Asn Gly Gly
 325 330 335

Asp Leu Met Phe His Met Gln Arg Gln Arg Lys Leu Pro Glu Glu His
 340 345 350

Ala Arg Phe Tyr Ala Ala Glu Ile Cys Ile Ala Leu Asn Phe Leu His
 355 360 365

Glu Arg Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu
 370 375 380

Asp Ala Asp Gly His Ile Lys Leu Thr Asp Tyr Gly Met Cys Lys Glu
 385 390 395 400

Gly Leu Gly Pro Gly Asp Thr Thr Ser Thr Phe Cys Gly Thr Pro Asn
 405 410 415

Tyr Ile Ala Pro Glu Ile Leu Arg Gly Glu Glu Tyr Gly Phe Ser Val
 420 425 430

Asp Trp Trp Ala Leu Gly Val Leu Met Phe Glu Met Met Ala Gly Arg
 435 440 445

Ser Pro Phe Asp Ile Ile Thr Asp Asn Pro Asp Met Asn Thr Glu Asp
 450 455 460

Tyr Leu Phe Gln Val Ile Leu Glu Lys Pro Ile Arg Ile Pro Arg Phe
 465 470 475 480

Leu Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp
 485 490 495

Pro Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile
 500 505 510

Lys Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys
 515 520 525

Lys Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly
 530 535 540

Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr
545 550 555 560

Pro Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu
565 570 575

Gly Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Thr Glu Glu Ser Val
580 585 590

<210> 3
<211> 3663
<212> DNA
<213> Homo sapiens

<220>
<223> phosphoinositide-specific phospholipase C beta 1,
isoform a (PLC-beta1), transcript variant 1

<400> 3
cagatggccg gggctcaacc cggagtgcac gccttgcaac tcaagcccggt gtgcgtgtcc 60
gacagcctca agaagggcac caaattcgta aagtggatg atgattcaac tattgttact 120
ccaaatttattt tgaggactga ccctcaggaa ttttctttt actggacaga tcaaaaacaag 180
gagacagagc tactggatct cagcctgtc aaagatgcca gatgtgggag acacgccaa 240
gctcccaagg accccaaattt acgtgaactt ttggatgtgg ggaacatcgg ggcgcctggag 300
cagcgcattga tcacagtggt gtatgggcct gacccctgtga acatctccca ttgaatctc 360
gtggctttcc aagaagaagt ggccaaggaa tggacaaatg aggttttcag ttggcaaca 420
aacctgctgg cccaaaacat gtccaggat gcatttctgg aaaaagccta tactaaactt 480
aagctgcaag tcactccaga agggcgtatt cctctcaaaa acatataatcg cttgtttca 540
gcagatcgga agcgagttga aactgctta gaggcttgcgt gtcttcatc ttcaaggaat 600
gattcaatac ctcaagaaga tttcactcca gaagtgtaca gagttttcct caacaacctt 660
tgccctcgac ctgaaattga taacatctt tcagaatttg gtgcaaaaag caaaccatat 720
cttaccgttg atcagatgtat ggattttatc aacctaaggc agcgagatcc tcggcttaat 780
gaaatactt atccacactt aaaaacaagag caagtccaaatg tattgattga gaagtatgaa 840
cccaacaaca gcctcgccag aaaaggacaa atatcagtgg atgggttcat gcgcstatctg 900
atggagaag aaaaacggagt cgtttcaccc gagaacttgcg atttgaatga agacatgtct 960
cagccccctt ctcactattt cattaattcc tcgcacaaca cctacccatc acgtggccaa 1020
ctggctggaa actcctctgt tgagatgtat cgccaaatgc tcctgtctgg ttgtcgctgt 1080
gtggagctgg actgctggaa gggacggact gcagaagagg aacctgtcat caccatggc 1140
ttcaccatga caactgaaat atcttcaag gaagtgtatc aagcaattgc ggagtgtgca 1200
ttaagactt cacctttcc aattctcattt tcgtttgaga accatgtgga ttccccaaag 1260
cagcaagccaa agatggcggaa gtactgcccga ctgatcttgc gggatccct tctcatggag 1320
ccctggaaa aatatccact ggaatctggat gttcctcttc caagccctat ggatttaatg 1380
tataaaaattt tggtgaaaaaa taagaagaaa tcacacaagt catcagaagg aagcggccaa 1440
aagaagctt cagaacaacgc ctccaaacacc tacagtgtact cctccagcat gttcgagccc 1500
tcatccccag gagccggaga agctgatacg gaaagtgcg acgacgtatc tgatgtatc 1560
tgtaaaaat cttcaatggat tgagggact gctggaaatg aggctatggc cacagaagaa 1620
atgtctaattc tggtgaacta tattcagccat gtcaagtttgc agtcatattgc aatttcaaaa 1680
aaaagaaata aaagtttgc aatgtctcc ttctgtggaaa ccaaaggact tgaacaactc 1740
accaagtctc cagtggaaatt tgtagaatat aacaaaatgc agcttagcag gatataatcca 1800
aaaggaacac gtgtggattc atccaactat atgcctcagc tcttctggaa tgcaggttgt 1860
cagatggatgg cacttaattt ccagacaatg gacccggctt tgcaaaataaa tatggggatg 1920
tatgaataca acgggaagag tggctacaga ttgaagccag agttcatgag gaggcctgac 1980
aagcattttg atccatttac tgaaggcatc gtagatggga tagtggccaa cactttgtct 2040
gttaagattt tttcaggatc gtttcttctt gataagaaatg ttggactta cgtggaaatg 2100
gatatgtttt gtttgcctgt ggatacaagg aggaaggcat ttaagaccaa aacatcccaa 2160
ggaaatgctg tgaatcctgt ctggaaagaa gaaaccttgc tttcaaaaaa ggtgggttctt 2220
cctactctgg cctgtttgag aatagcagtt tatgaagaag gaggtaaattt cattggccac 2280
cgtatcttgc cagtgcacgc cattcggccaa ggctatcact atatctgtct aaggaatgaa 2340
aggaaccagc ctctgacgct gcctgctgtc tttgtctaca tagaagtgaa agactatgtg 2400
ccagacacat atgcagatgt catgcacatc ttatcaaacc caatccgata tgcacatctg 2460

atggaacaga gagctaagca attggctgct ttgacactgg aagatgaaga agaagtaaag 2520
 aaagaggctg atcctggaga aacaccatca gaggctcaa gtgaagcgag aacgactcca 2580
 gcagaaaatg gggtaatca cactacaacc ctgacaccca agccacccctc ccaggctctc 2640
 cacagccagc cagctccagg ttctgtaaag gcacctgcca aaacagaaga tcttattcag 2700
 agtgtcttaa cagaagtgg agcacagacc atcagaagaac taaagcaaca gaaatcgaaa 2760
 gtgaaacttc aaaagaaaca ctacaaagaa atgaaagacc tggtaagag acaccacaag 2820
 aaaaccactg accttatcaa agaacacact accaagtata atgaaattca gaatgactac 2880
 ttgagaagga gagccgctt ggaaaagtcc gccaaaagg acagtaagaa aaaatcgaaa 2940
 cccagcagcc ctgatcatgg ttcatcaacg attgagcaag acctcgctgc tctggatgct 3000
 gaaatgaccc aaaagttaa agacttgg gacaaacaac agcagcagct gcttaatctt 3060
 cggcaagaac agtattatag taaaaatac cagaagcgag aacatattaa actgcttatt 3120
 caaaagttga cggatgtcgc agaagagtgt cagaacaatc agttaaagaa gctcaaagaa 3180
 atctgtgaga aagaaaagaa agaattaaag aagaaaatgg ataaaaagag gcaggagaag 3240
 ataacagaag ctaaatccaa agacaaaagt cagatggaaaggagaaagac agagatgatc 3300
 cggtcatata tccaggaagt ggtgcagttt atcaagaggc tagaagaagc gcaaagtaaa 3360
 cggcaagaaa aactcgtaga gaaacacaag gaaatacgctc agcagatcctt ggtgaaaag 3420
 cccaagctgc aggtggagct ggagcaagaa tccaagaca aattcaaaag actgcccctc 3480
 gagatttgg aattcgtgca ggaagccatg aaaggaaaga tcagtgaaga cagcaatcac 3540
 gttctgccc ctctccctt gtcctcagac cctggaaaag tgaaccacaa gactccctcc 3600
 agtgaggagc tgggaggaga catcccagga aaagaatttg atactcctct gtgaatgctc 3660
 ctg 3663

<210> 4
 <211> 1216
 <212> PRT
 <213> Homo sapiens

<220>
 <223> phosphoinositide-specific phospholipase C beta 1,
 isoform a (PLC-beta1), transcript variant 1

<400> 4
 Met Ala Gly Ala Gln Pro Gly Val His Ala Leu Gln Leu Lys Pro Val
 1 5 10 15

Cys Val Ser Asp Ser Leu Lys Lys Gly Thr Lys Phe Val Lys Trp Asp
 20 25 30

Asp Asp Ser Thr Ile Val Thr Pro Ile Ile Leu Arg Thr Asp Pro Gln
 35 40 45

Gly Phe Phe Phe Tyr Trp Thr Asp Gln Asn Lys Glu Thr Glu Leu Leu
 50 55 60

Asp Leu Ser Leu Val Lys Asp Ala Arg Cys Gly Arg His Ala Lys Ala
 65 70 75 80

Pro Lys Asp Pro Lys Leu Arg Glu Leu Leu Asp Val Gly Asn Ile Gly
 85 90 95

Arg Leu Glu Gln Arg Met Ile Thr Val Val Tyr Gly Pro Asp Leu Val
 100 105 110

Asn Ile Ser His Leu Asn Leu Val Ala Phe Gln Glu Val Ala Lys
 115 120 125

Glu Trp Thr Asn Glu Val Phe Ser Leu Ala Thr Asn Leu Leu Ala Gln
 130 135 140

Asn	Met	Ser	Arg	Asp	Ala	Phe	Leu	Glu	Lys	Ala	Tyr	Thr	Lys	Leu	Lys
145					150				155					160	
Leu	Gln	Val	Thr	Pro	Glu	Gly	Arg	Ile	Pro	Leu	Lys	Asn	Ile	Tyr	Arg
				165					170				175		
Leu	Phe	Ser	Ala	Asp	Arg	Lys	Arg	Val	Glu	Thr	Ala	Leu	Glu	Ala	Cys
			180			185						190			
Ser	Leu	Pro	Ser	Ser	Arg	Asn	Asp	Ser	Ile	Pro	Gln	Glu	Asp	Phe	Thr
			195				200				205				
Pro	Glu	Val	Tyr	Arg	Val	Phe	Leu	Asn	Asn	Leu	Cys	Pro	Arg	Pro	Glu
	210				215					220					
Ile	Asp	Asn	Ile	Phe	Ser	Glu	Phe	Gly	Ala	Lys	Ser	Lys	Pro	Tyr	Leu
	225				230				235			240			
Thr	Val	Asp	Gln	Met	Met	Asp	Phe	Ile	Asn	Leu	Lys	Gln	Arg	Asp	Pro
			245			250				255					
Arg	Leu	Asn	Glu	Ile	Leu	Tyr	Pro	Pro	Leu	Lys	Gln	Glu	Gln	Val	Gln
			260				265			270					
Val	Leu	Ile	Glu	Lys	Tyr	Glu	Pro	Asn	Asn	Ser	Leu	Ala	Arg	Lys	Gly
			275			280				285					
Gln	Ile	Ser	Val	Asp	Gly	Phe	Met	Arg	Tyr	Leu	Ser	Gly	Glu	Glu	Asn
	290				295					300					
Gly	Val	Val	Ser	Pro	Glu	Lys	Leu	Asp	Leu	Asn	Glu	Asp	Met	Ser	Gln
	305				310				315			320			
Pro	Leu	Ser	His	Tyr	Phe	Ile	Asn	Ser	Ser	His	Asn	Thr	Tyr	Leu	Thr
			325				330				335				
Ala	Gly	Gln	Leu	Ala	Gly	Asn	Ser	Ser	Val	Glu	Met	Tyr	Arg	Gln	Val
			340				345				350				
Leu	Leu	Ser	Gly	Cys	Arg	Cys	Val	Glu	Leu	Asp	Cys	Trp	Lys	Gly	Arg
			355			360				365					
Thr	Ala	Glu	Glu	Pro	Val	Ile	Thr	His	Gly	Phe	Thr	Met	Thr	Thr	
	370				375					380					
Glu	Ile	Ser	Phe	Lys	Glu	Val	Ile	Glu	Ala	Ile	Ala	Glu	Cys	Ala	Phe
	385				390				395			400			
Lys	Thr	Ser	Pro	Phe	Pro	Ile	Leu	Leu	Ser	Phe	Glu	Asn	His	Val	Asp
			405				410				415				
Ser	Pro	Lys	Gln	Gln	Ala	Lys	Met	Ala	Glu	Tyr	Cys	Arg	Leu	Ile	Phe
			420			425				430					
Gly	Asp	Ala	Leu	Leu	Met	Glu	Pro	Leu	Glu	Lys	Tyr	Pro	Leu	Glu	Ser
			435			440				445					
Gly	Val	Pro	Leu	Pro	Ser	Pro	Met	Asp	Leu	Met	Tyr	Lys	Ile	Leu	Val
	450				455				460						

Lys Asn Lys Lys Lys Ser His Lys Ser Ser Glu Gly Ser Gly Lys Lys
 465 470 475 480

Lys Leu Ser Glu Gln Ala Ser Asn Thr Tyr Ser Asp Ser Ser Met
 485 490 495

Phe Glu Pro Ser Ser Pro Gly Ala Gly Glu Ala Asp Thr Glu Ser Asp
 500 505 510

Asp Asp Asp Asp Asp Asp Cys Lys Lys Ser Ser Met Asp Glu Gly
 515 520 525

Thr Ala Gly Ser Glu Ala Met Ala Thr Glu Glu Met Ser Asn Leu Val
 530 535 540

Asn Tyr Ile Gln Pro Val Lys Phe Glu Ser Phe Glu Ile Ser Lys Lys
 545 550 555 560

Arg Asn Lys Ser Phe Glu Met Ser Ser Phe Val Glu Thr Lys Gly Leu
 565 570 575

Glu Gln Leu Thr Lys Ser Pro Val Glu Phe Val Glu Tyr Asn Lys Met
 580 585 590

Gln Leu Ser Arg Ile Tyr Pro Lys Gly Thr Arg Val Asp Ser Ser Asn
 595 600 605

Tyr Met Pro Gln Leu Phe Trp Asn Ala Gly Cys Gln Met Val Ala Leu
 610 615 620

Asn Phe Gln Thr Met Asp Leu Ala Met Gln Ile Asn Met Gly Met Tyr
 625 630 635 640

Glu Tyr Asn Gly Lys Ser Gly Tyr Arg Leu Lys Pro Glu Phe Met Arg
 645 650 655

Arg Pro Asp Lys His Phe Asp Pro Phe Thr Glu Gly Ile Val Asp Gly
 660 665 670

Ile Val Ala Asn Thr Leu Ser Val Lys Ile Ile Ser Gly Gln Phe Leu
 675 680 685

Ser Asp Lys Lys Val Gly Thr Tyr Val Glu Val Asp Met Phe Gly Leu
 690 695 700

Pro Val Asp Thr Arg Arg Lys Ala Phe Lys Thr Lys Thr Ser Gln Gly
 705 710 715 720

Asn Ala Val Asn Pro Val Trp Glu Glu Glu Pro Ile Val Phe Lys Lys
 725 730 735

Val Val Leu Pro Thr Leu Ala Cys Leu Arg Ile Ala Val Tyr Glu Glu
 740 745 750

Gly Gly Lys Phe Ile Gly His Arg Ile Leu Pro Val Gln Ala Ile Arg
 755 760 765

Pro Gly Tyr His Tyr Ile Cys Leu Arg Asn Glu Arg Asn Gln Pro Leu
 770 775 780

Thr	Leu	Pro	Ala	Val	Phe	Val	Tyr	Ile	Glu	Val	Lys	Asp	Tyr	Val	Pro	
785					790				795					800		
Asp	Thr	Tyr	Ala	Asp	Val	Ile	Glu	Ala	Leu	Ser	Asn	Pro	Ile	Arg	Tyr	
					805				810				815			
Val	Asn	Leu	Met	Glu	Gln	Arg	Ala	Lys	Gln	Leu	Ala	Ala	Leu	Thr	Leu	
					820				825				830			
Glu	Asp	Glu	Glu	Glu	Val	Lys	Lys	Glu	Ala	Asp	Pro	Gly	Glu	Thr	Pro	
					835				840			845				
Ser	Glu	Ala	Pro	Ser	Glu	Ala	Arg	Thr	Thr	Pro	Ala	Glu	Asn	Gly	Val	
					850				855			860				
Asn	His	Thr	Thr	Leu	Thr	Pro	Lys	Pro	Pro	Ser	Gln	Ala	Leu	His		
					865				870			875		880		
Ser	Gln	Pro	Ala	Pro	Gly	Ser	Val	Lys	Ala	Pro	Ala	Lys	Thr	Glu	Asp	
					885				890			895				
Leu	Ile	Gln	Ser	Val	Leu	Thr	Glu	Val	Glu	Ala	Gln	Thr	Ile	Glu	Glu	
					900				905			910				
Leu	Lys	Gln	Gln	Lys	Ser	Phe	Val	Lys	Leu	Gln	Lys	Lys	His	Tyr	Lys	
					915				920			925				
Glu	Met	Lys	Asp	Leu	Val	Lys	Arg	His	His	Lys	Lys	Thr	Thr	Asp	Leu	
					930				935			940				
Ile	Lys	Glu	His	Thr	Thr	Lys	Tyr	Asn	Glu	Ile	Gln	Asn	Asp	Tyr	Leu	
					945				950			955		960		
Arg	Arg	Arg	Ala	Ala	Leu	Glu	Lys	Ser	Ala	Lys	Lys	Asp	Ser	Lys	Lys	
					965				970			975				
Lys	Ser	Glu	Pro	Ser	Ser	Pro	Asp	His	Gly	Ser	Ser	Thr	Ile	Glu	Gln	
					980				985			990				
Asp	Leu	Ala	Ala	Leu	Asp	Ala	Glu	Met	Thr	Gln	Lys	Leu	Ile	Asp	Leu	
					995				1000			1005				
Lys	Asp	Lys	Gln	Gln	Gln	Leu	Leu	Asn	Leu	Arg	Gln	Glu	Gln	Tyr		
					1010				1015			1020				
Tyr	Ser	Glu	Lys	Tyr	Gln	Lys	Arg	Glu	His	Ile	Lys	Leu	Ile	Gln		
					1025				1030			1035		1040		
Lys	Leu	Thr	Asp	Val	Ala	Glu	Glu	Cys	Gln	Asn	Asn	Gln	Leu	Lys	Lys	
					1045				1050			1055				
Leu	Lys	Glu	Ile	Cys	Glu	Lys	Glu	Lys	Glu	Leu	Lys	Lys	Met			
					1060				1065			1070				
Asp	Lys	Lys	Arg	Gln	Glu	Lys	Ile	Thr	Glu	Ala	Lys	Ser	Lys	Asp	Lys	
					1075				1080			1085				
Ser	Gln	Met	Glu	Glu	Glu	Lys	Thr	Glu	Met	Ile	Arg	Ser	Tyr	Ile	Gln	
					1090				1095			1100				

Glu Val Val Gln Tyr Ile Lys Arg Leu Glu Ala Gln Ser Lys Arg
1105 1110 1115 1120

Gln Glu Lys Leu Val Glu Lys His Lys Glu Ile Arg Gln Gln Ile Leu
1125 1130 1135

Asp Glu Lys Pro Lys Leu Gln Val Glu Leu Glu Gln Glu Tyr Gln Asp
1140 1145 1150

Lys Phe Lys Arg Leu Pro Leu Glu Ile Leu Glu Phe Val Gln Glu Ala
1155 1160 1165

Met Lys Gly Lys Ile Ser Glu Asp Ser Asn His Gly Ser Ala Pro Leu
1170 1175 1180

Ser Leu Ser Ser Asp Pro Gly Lys Val Asn His Lys Thr Pro Ser Ser
1185 1190 1195 1200

Glu Glu Leu Gly Asp Ile Pro Gly Lys Glu Phe Asp Thr Pro Leu
1205 1210 1215

<210> 5
<211> 3052

<212> DNA

<213> Homo sapiens

<220>

<223> cytoplasmic tyrosine kinase focal adhesion kinase
(FAK)

<400> 5

ccggtgtgaa ggcctatggat gattactggg ttgttggaaa gaagtctaac tatgaagtat 60
tagaaaaaga tgggttta aagcgattt ttccataagag ttactggat tctgtcaagg 120
ccaaaacact aagaaaactg atccaacaaa catttagaca atttgccaaac cttaatagag 180
aagaaaagtat tctgaaattc tttgagatcc tgcgtccagt ctacagattt gataaggaat 240
gcttcaggat tgctcttggt tcaagctgga ttatccatgtt ggaacttggca atcggccca 300
aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatctt gctgacttca 360
ctcaagtgc aaccatttcg tattcaaaaca gtgaagacaa ggacagaaaa ggaatgctac 420
aactaaaaat agcaggtgca cccgagcctc tgacagtgc ggcaccatcc ctaaccattt 480
cgagaaataat ggctgaccta atagatgggt actgcccggct ggtgaatggc acctcgccagt 540
catttatcat cagaccttcg aaagaagtg aacggggctt gccatcaata ccaaagttgg 600
ccaaacagcga aaagcaaggc atgcggacac acggccgtctc tgcgtcagaa acagatgatt 660
atgctgagat tatagatgaa gaagatactt acaccatgcc ctcaccagg gattatgaga 720
ttcaaaagaga aagaatagaa cttggacatgtt gatggaga aggccattt ggagatgtac 780
atcaaggcat ttatatgatcc ccagagaatc cagctttggc ggttgcattt aaaaatgtt 840
aaaaactgtac ttccggacagc gtgagagaga aatttcttca agaagcctgc cattacacat 900
ctttgcactg gaatttggtc agatataaa gtatccctaa tggatgtcc tgcccgacacc 960
ccaggaatgc agagttacaatc atgcgtcaatgtt tggaccatcc tcatattgtt aagctgattt 1020
gagtcatcac agagaatcct gtctggataa tcatggagct gtgcacactt ggagagctga 1080
ggtcattttt gcaagtaagg aaatacagtt tggatcttagc atctttgatc ctgtatgcct 1140
atcagcttag tacagctctt gcataatctg agagcaaaatg atttgcac accgacattt 1200
ctgctcgaa tggatgttgc tcctcaatgtt attgtgtttt attaggagac tttggatttt 1260
cccgatataat ggaagatagt acttactaca aagttccaa aggaaaatttgc cttatataat 1320
ggatggctcc agagtcaatc aattttcgac gtttacctc agctgtgc gtatggatgt 1380
ttgggtgttgc tatgtggag atactgtgc atgtgtgaa gcctttcaa ggagtgaaga 1440
acaatgtatgtt aatcggtcga attgaaaatg gggaaagattt accaatgcctt ccaaatttgc 1500
ctccatccctt ctacagccctt atgacgaaat gctggcccta tgacccagc aggccggccca 1560
ggtttactgaa acttaaagct cagctcagca caatcctgga ggaagagaag gctcagcaag 1620
aagagcgtat gaggatggag tccagaagac aggccacagt gtcctggac tccggaggtt 1680
ctgtatgttgc accggcccaatc cccagcagac cgggttatcc cagtcggaggc tccagcgaag 1740

gattttatcc cagccccacag cacatggtagt aaaccaatca ttaccagggtt tctggctacc 1800
 ctggttcaca tggaaatcaca gccatggctg gcagcatcta tccaggtcag gcatctctt 1860
 tggaccaaac agattcatgg aatcatagat ctcaggagat agcaatgtgg cagcccaatg 1920
 tggaggactc tacagtattg gacctgcgag ggattggca agtggccca acccatctga 1980
 tggaaagagcg tctaattccga cagcaacagg aaatggaaaga agatcagcgc tggctggaaa 2040
 aagagggaaag atttctgatt gggaaaccaac atatatatca gcctgtgggt aaaccagatc 2100
 ctgcagctcc accaaagaaaa ccgcctcgcc ctggagctcc cggtcatctg ggaagccttg 2160
 ccagcctcag cagccctgct gacagctaca acgagggtgt caagcttcag ccccgaggaaa 2220
 tcagcccccc tcctactgccc aacctggacc ggtcaatga taaggtgtac gagaatgtga 2280
 cgggcctggt gaaagctgtc atcgagatgt ccagtaaaat ccagccagcc ccaaccagagg 2340
 agtatgtccc tatggtgaag gaagtcgct tggccctgag gacattattg gccactgtgg 2400
 atgagaccat tcccctcta ccagccagca cccaccgaga gattgagatg gcacagaagc 2460
 tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccg cagtatgtca 2520
 tgaccagcc ccagcaagag tacaaaaaagc aaatgtgac tgccgctcac gccctggctg 2580
 tggatgccaa aaacttactc gatgtcattt accaagcaag actgaaaatg cttggccaga 2640
 cgagaccaca ctgagccctcc ccttaggagca cgtcttgcta ccctctttg aagatgttct 2700
 cttagccttcc accagcagcg aggaattaac cctgtgtcct cagtcgccc cactcacagc 2760
 tccaactttt ttgaatgacc atctggttga aaaatcttc tcatataagt ttaaccacac 2820
 tttgatttgg gttcattttt tgttttgtt tttcaatca tgatattcag aaaaatccag 2880
 gatccaaaat gtggcggttt tctaagaatg aaaattatat gtaagcttt aagcatcatg 2940
 aagaacaatt tatgttcaca ttaagatacg ttctaaaggg ggtatggccaa ggggtgacat 3000
 cttaatttcctt aaactacctt agctgcata gggaaat tc 3052

<210> 6
 <211> 879
 <212> PRT
 <213> Homo sapiens

<220>
 <223> cytoplasmic tyrosine kinase focal adhesion kinase
 (FAK)

<400> 6
 Met Ser Asp Tyr Trp Val Val Gly Lys Lys Ser Asn Tyr Glu Val Leu
 1 5 10 15

Glu Lys Asp Val Gly Leu Lys Arg Phe Phe Pro Lys Ser Leu Leu Asp
 20 25 30

Ser Val Lys Ala Lys Thr Leu Arg Lys Leu Ile Gln Gln Thr Phe Arg
 35 40 45

Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser Ile Leu Lys Phe Phe Glu
 50 55 60

Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu Cys Phe Lys Cys Ala
 65 70 75 80

Leu Gly Ser Ser Trp Ile Ile Ser Val Glu Leu Ala Ile Gly Pro Glu
 85 90 95

Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys Asn Pro Thr His Leu
 100 105 110

Ala Asp Phe Thr Gln Val Gln Thr Ile Gln Tyr Ser Asn Ser Glu Asp
 115 120 125

Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile Ala Gly Ala Pro Glu
 130 135 140

Pro Leu Thr Val Thr Ala Pro Ser Leu Thr Ile Ala Glu Asn Met Ala
 145 150 155 160
 Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val Asn Gly Thr Ser Gln Ser
 165 170 175
 Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu Arg Ala Leu Pro Ser Ile
 180 185 190
 Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly Met Arg Thr His Ala Val
 195 200 205
 Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu Ile Ile Asp Glu Glu Asp
 210 215 220
 Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr Glu Ile Gln Arg Glu Arg
 225 230 235 240
 Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly Gln Phe Gly Asp Val His
 245 250 255
 Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro Ala Leu Ala Val Ala Ile
 260 265 270
 Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser Val Arg Glu Lys Phe Leu
 275 280 285
 Gln Glu Ala Cys His Tyr Thr Ser Leu His Trp Asn Trp Cys Arg Tyr
 290 295 300
 Ile Ser Asp Pro Asn Val Asp Ala Cys Pro Asp Pro Arg Asn Ala Glu
 305 310 315 320
 Leu Thr Met Arg Gln Phe Asp His Pro His Ile Val Lys Leu Ile Gly
 325 330 335
 Val Ile Thr Glu Asn Pro Val Trp Ile Ile Met Glu Leu Cys Thr Leu
 340 345 350
 Gly Glu Leu Arg Ser Phe Leu Gln Val Arg Lys Tyr Ser Leu Asp Leu
 355 360 365
 Ala Ser Leu Ile Leu Tyr Ala Tyr Gln Leu Ser Thr Ala Leu Ala Tyr
 370 375 380
 Leu Glu Ser Lys Arg Phe Val His Arg Asp Ile Ala Ala Arg Asn Val
 385 390 395 400
 Leu Val Ser Ser Asn Asp Cys Val Lys Leu Gly Asp Phe Gly Leu Ser
 405 410 415
 Arg Tyr Met Glu Asp Ser Thr Tyr Tyr Lys Ala Ser Lys Gly Lys Leu
 420 425 430
 Pro Ile Lys Trp Met Ala Pro Glu Ser Ile Asn Phe Arg Arg Phe Thr
 435 440 445
 Ser Ala Ser Asp Val Trp Met Phe Gly Val Cys Met Trp Glu Ile Leu
 450 455 460

Met His Gly Val Lys Pro Phe Gln Gly Val Lys Asn Asn Asp Val Ile
 465 470 475 480

Gly Arg Ile Glu Asn Gly Glu Arg Leu Pro Met Pro Pro Asn Cys Pro
 485 490 495

Pro Thr Leu Tyr Ser Leu Met Thr Lys Cys Trp Ala Tyr Asp Pro Ser
 500 505 510

Arg Arg Pro Arg Phe Thr Glu Leu Lys Ala Gln Leu Ser Thr Ile Leu
 515 520 525

Glu Glu Glu Lys Ala Gln Gln Glu Glu Arg Met Arg Met Glu Ser Arg
 530 535 540

Arg Gln Ala Thr Val Ser Trp Asp Ser Gly Gly Ser Asp Glu Ala Pro
 545 550 555 560

Pro Lys Pro Ser Arg Pro Gly Tyr Pro Ser Pro Arg Ser Ser Glu Gly
 565 570 575

Phe Tyr Pro Ser Pro Gln His Met Val Gln Thr Asn His Tyr Gln Val
 580 585 590

Ser Gly Tyr Pro Gly Ser His Gly Ile Thr Ala Met Ala Gly Ser Ile
 595 600 605

Tyr Pro Gly Gln Ala Ser Leu Leu Asp Gln Thr Asp Ser Trp Asn His
 610 615 620

Arg Ser Gln Glu Ile Ala Met Trp Gln Pro Asn Val Glu Asp Ser Thr
 625 630 635 640

Val Leu Asp Leu Arg Gly Ile Gly Gln Val Leu Pro Thr His Leu Met
 645 650 655

Glu Glu Arg Leu Ile Arg Gln Gln Glu Met Glu Glu Asp Gln Arg
 660 665 670

Trp Leu Glu Lys Glu Glu Arg Phe Leu Ile Gly Asn Gln His Ile Tyr
 675 680 685

Gln Pro Val Gly Lys Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro
 690 695 700

Arg Pro Gly Ala Pro Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser
 705 710 715 720

Pro Ala Asp Ser Tyr Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile
 725 730 735

Ser Pro Pro Pro Thr Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr
 740 745 750

Glu Asn Val Thr Gly Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys
 755 760 765

Ile Gln Pro Ala Pro Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val
 770 775 780

Gly Leu Ala Leu Arg Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro
785 790 795 800

Leu Leu Pro Ala Ser Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu
805 810 815

Leu Asn Ser Asp Leu Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln
820 825 830

Gln Tyr Val Met Thr Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu
835 840 845

Thr Ala Ala His Ala Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val
850 855 860

Ile Asp Gln Ala Arg Leu Lys Met Leu Gly Gln Thr Arg Pro His
865 870 875

<210> 7
<211> 4089
<212> DNA
<213> Homo sapiens

<220>
<223> calcium dependent tyrosine kinase focal adhesion
kinase 2 (FAK2)

<400> 7
gaattccgtc agccctttta ctcagccaca gcctccggag ccgttgcaca cctacctgcc 60
cgcccgactt acctgtactt gccgcgtcc cggctcacct ggcggtgccc gaggagtagt 120
cgctggagtc cgccgcctccc tgggactgca atgtgccat cttagctgt gcctgagagg 180
atgtctgggg tgcggagcc cctgagtcga gtaaagtgg gcacgttacg cccgcctgaa 240
ggccctgcag agcccatggg ggtggtacca gtagatgtgg aaaaggagga cgtgcgtatc 300
ctcaaggtct gcttctatag caacagcttc aatcctggga aaaactcaa actggtcaaa 360
tgcactgtcc agacggagat cccggagatc atcacctcca tcctgctgag cgggcggatc 420
ggcccaaca tccgggtggc tgagtgtat gggctgaggc tgaagcacat gaagtccgat 480
gagatccact ggctgcaccc acagatgacg gtgggtgagg tgcaggacaa gtatgagtgt 540
ctgcacgtgg aagccgagtg gaggtatgac ctccaaatcc gctacttgcc agaagacttc 600
atggagagcc tgaaggagga caggaccacg ctgtctatt ttaccacaca gctccggAAC 660
gactacatgc agcgctacgc cagcaaggc acgaggggca tggccctgca gctgggctgc 720
ctggagctca ggcgggtctt caaggatatg cccacaatg cacttgacaa gaagtccaaac 780
ttcgagctcc tagaaaagga agtggggctg gacttgggg tcccaaagca gatgcaggag 840
aacttaaagc ccaaacagtt ccggaagatg atccagcaga cttccagca gtacgcctcg 900
ctcaggggagg aggagtgcgt catgaagttc ttcaacactc tgcggccgtt cgccaaacatc 960
gaccaggaga cttaccgctg tgaactcatt caaggatgga acattactgt ggacctggc 1020
atggcccta aaggatccg ccagctgact agtcaggacg caaagccac ctgcctggcc 1080
gagttcaagc agatcaggc catcagggtc ctcccgctgg aggaggccca ggcagtactt 1140
cagctggcgt ttgaagggtc ccccccagcc ttgtccatca aaacctcatc cctagcagag 1200
gctgagaaca tggctgaccc catagacggc tactgccggc tgcagggtga gcaccaaggc 1260
tctctcatca tccatcctag gaaagatgtt gagaagcgga acagcctgcc ccagatcccc 1320
atgctaaacc tggaggccccg gcggtccac ctctcagaga gctgcagcat agagtcagac 1380
atctacgcag agattcccga cggaaaccctg cgaaggccccg gaggtccaca gtatggcatt 1440
gccccgtgaag atgtggtcct gaatcgatatt ctggggaaag gctttttgg ggaggtctat 1500
gaaggtgtct acacaaaatca taaaggggag aaaatcaatg tagctgtcaa gacctgcaag 1560
aaagactgca ctctggacaa caaggagaag ttcatgagcg aggcaatgtat catgaagaaac 1620
ctcgaccacc cgcacatcgt gaagctgatc ggcacatcattt aagaggagcc cacctggatc 1680
atcatgaaat tgcggatcc tggggagctg ggcacactacc tggagcggaa caagaactcc 1740
ctgaaggtgc tcaccctcgt gctgtactca ctgcagatat gcaaagccat ggcctacctg 1800
gagagcatca actgcgtgca cagggacatt gctgtccggaa acatcctgggt ggcctccct 1860
gagtggtgtga agctggggga ctgggtctt tccggatca ttgaggacga ggactattac 1920

aaaggctctg tgactcgtct ccccatcaaa tggatgtccc cagagtc当地 1980
cgcttcacga cagccagtga cgtctggat ttcggctgtgt gcatgtggaa gatcctgagc 2040
tttggaaaggc agcccttctt ctggctggag aacaaggatg tcatcggtt gctggagaaa 2100
ggagaccggc tgcccaagcc tgatctctgt ccaccgggtcc tttataccct catgaccgc 2160
tgctggact acgaccccaag tgaccggccc cgcttcaccg agctgggtg cagcctcagt 2220
gacgtttatac agatggagaa ggacattgcc atggagcaag agaggaatgc tcgctaccga 2280
acccccaat tcttggagcc cacagccttc cagaacccc cacccttcc cagccgaccc 2340
aagtacagac cccctccgca aaccaacccct ctggctccaa agctgcagtt ccagggttcc 2400
gagggtctgt gtgcagcctc tcctacgctc accaccctta tggagtatcc atctcccg 2460
aactcaactgc acaccccaacc tttccacccgg cacaatgtct tcaaaccgcca cagcatgggg 2520
gaggaggact tcatccaacc cagcagccga gaagaggccc agcagctgtg ggaggctgaa 2580
aaggtaaaa tgcggcaat cctggacaaa cagcagaagc agatgggtgaa ggactaccag 2640
tgctcaggc aggaggagaa gttccctggac cccatggttt atatgaatga taagtcccc 2700
ttgacgcccag agaaggaggt cggctacccg gagttcacag ggccccccaca gaagccccccg 2760
agctggcg cacagtccat ccagccaca gctaaccctgg accggaccga tgacctgg 2820
tacctcaatg tcatggagct ggtgcgggccc gtgctggagc tcaagaatga gctctgtc 2880
ctgcccccccg agggctacgt ggtgggtgtg aagaatgtgg ggctgaccctt ggggaagctc 2940
atcggggagcg tggatgtatc cctgccttcc ttggcgtcat cttcacggac agagatcgag 3000
ggcacccaga aactgctcaa caaagacctg gcagagctca tcaacaatg gggctggcg 3060
cagcagaacg ccgtgacccctc cctgagtgag gagtgcaga ggcagatgct gacggcttca 3120
cacaccctgg ctgtggacgc caagaacctg ctcgacgctg tggaccaggc caaggttctg 3180
gccaatctgg cccacccacc tgcagagtg cggagggtgg gggccacccctg cctgcgtt 3240
ccgccccctgc ctgcacatgtc cttcccttgc cttgctgtt gtcatgtggg tttccagg 3300
agaaggccaa ggggagtcac cttcccttgc cactttgcac gacccctctt ccccacccct 3360
acccctggct gtactgctca ggctgcagct ggacagaggg gactctggc tatggacaca 3420
gggtgacggt gacaagatg gtcagaggg ggactgctgc tgcctggcca ctgctccct 3480
agccagccctg gtccatgcag ggggctctg ggggtgggaa ggtgtcacat ggtgcccct 3540
gccttatata tggacatggc aggccgattt gggaaaccaag ctattccctt ccctccct 3600
tctccctca gatgtccctt gatgcacaga gaagctgggg aggagctttt tttccgggg 3660
tcaggcagcc agtgagatga gggatggcc tggcattttt gtacagtgtt tattgaaatt 3720
tatttaatgt gaggtttggc ctggactgac agcatgtgcc ctccctgagg aggaccagg 3780
cacagtccag gaacaagcta attgggagtc cagcacagg atgctgtttt gtcacaaac 3840
caagcatcag ggggagaagc cagagagatg cggccaaagat aggaccttgg gccaaatccg 3900
ctctcttcctt gcccctctt ctcttcctt cttactttt cttgctttt ccctctttt 3960
ttactcctcc tctttctctc ccccacccccc attctcatct gcaccccttctt tttctcatgt 4020
gtttgcataa acattttttt aacttcttcc tatttgactt gtgggtgaat taaaattgtc 4080
ccatttgca 4089

<210> 8
<211> 1009
<212> PRT
<213> Homo sapiens

<220>
<223> calcium dependent tyrosine kinase focal adhesion
kinase 2 (FAK2)

<400> 8
Met Ser Gly Val Ser Glu Pro Leu Ser Arg Val Lys Leu Gly Thr Leu
1 5 10 15

Arg Arg Pro Glu Gly Pro Ala Glu Pro Met Val Val Val Pro Val Asp
20 25 30

Val Glu Lys Glu Asp Val Arg Ile Leu Lys Val Cys Phe Tyr Ser Asn
35 40 45

Ser Phe Asn Pro Gly Lys Asn Phe Lys Leu Val Lys Cys Thr Val Gln
50 55 60

Thr Glu Ile Arg Glu Ile Ile Thr Ser Ile Leu Leu Ser Gly Arg Ile
 65 70 75 80
 Gly Pro Asn Ile Arg Leu Ala Glu Cys Tyr Gly Leu Arg Leu Lys His
 85 90 95
 Met Lys Ser Asp Glu Ile His Trp Leu His Pro Gln Met Thr Val Gly
 100 105 110
 Glu Val Gln Asp Lys Tyr Glu Cys Leu His Val Glu Ala Glu Trp Arg
 115 120 125
 Tyr Asp Leu Gln Ile Arg Tyr Leu Pro Glu Asp Phe Met Glu Ser Leu
 130 135 140
 Lys Glu Asp Arg Thr Thr Leu Leu Tyr Phe Tyr Gln Gln Leu Arg Asn
 145 150 155 160
 Asp Tyr Met Gln Arg Tyr Ala Ser Lys Val Ser Glu Gly Met Ala Leu
 165 170 175
 Gln Leu Gly Cys Leu Glu Leu Arg Arg Phe Phe Lys Asp Met Pro His
 180 185 190
 Asn Ala Leu Asp Lys Lys Ser Asn Phe Glu Leu Leu Glu Lys Glu Val
 195 200 205
 Gly Leu Asp Leu Phe Phe Pro Lys Gln Met Gln Glu Asn Leu Lys Pro
 210 215 220
 Lys Gln Phe Arg Lys Met Ile Gln Gln Thr Phe Gln Gln Tyr Ala Ser
 225 230 235 240
 Leu Arg Glu Glu Glu Cys Val Met Lys Phe Phe Asn Thr Leu Ala Gly
 245 250 255
 Phe Ala Asn Ile Asp Gln Glu Thr Tyr Arg Cys Glu Leu Ile Gln Gly
 260 265 270
 Trp Asn Ile Thr Val Asp Leu Val Ile Gly Pro Lys Gly Ile Arg Gln
 275 280 285
 Leu Thr Ser Gln Asp Ala Lys Pro Thr Cys Leu Ala Glu Phe Lys Gln
 290 295 300
 Ile Arg Ser Ile Arg Cys Leu Pro Leu Glu Glu Gly Gln Ala Val Leu
 305 310 315 320
 Gln Leu Gly Ile Glu Gly Ala Pro Gln Ala Leu Ser Ile Lys Thr Ser
 325 330 335
 Ser Leu Ala Glu Ala Glu Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys
 340 345 350
 Arg Leu Gln Gly Glu His Gln Gly Ser Leu Ile Ile His Pro Arg Lys
 355 360 365
 Asp Gly Glu Lys Arg Asn Ser Leu Pro Gln Ile Pro Met Leu Asn Leu
 370 375 380

Glu Ala Arg Arg Ser His Leu Ser Glu Ser Cys Ser Ile Glu Ser Asp
 385 390 395 400
 Ile Tyr Ala Glu Ile Pro Asp Glu Thr Leu Arg Arg Pro Gly Gly Pro
 405 410 415
 Gln Tyr Gly Ile Ala Arg Glu Asp Val Val Leu Asn Arg Ile Leu Gly
 420 425 430
 Glu Gly Phe Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn His Lys
 435 440 445
 Gly Glu Lys Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp Cys Thr
 450 455 460
 Leu Asp Asn Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met Lys Asn
 465 470 475 480
 Leu Asp His Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu Glu
 485 490 495
 Pro Thr Trp Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu Gly His
 500 505 510
 Tyr Leu Glu Arg Asn Lys Asn Ser Leu Lys Val Leu Thr Leu Val Leu
 515 520 525
 Tyr Ser Leu Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser Ile Asn
 530 535 540
 Cys Val His Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala Ser Pro
 545 550 555 560
 Glu Cys Val Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile Glu Asp
 565 570 575
 Glu Asp Tyr Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys Trp Met
 580 585 590
 Ser Pro Glu Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser Asp Val
 595 600 605
 Trp Met Phe Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly Lys Gln
 610 615 620
 Pro Phe Phe Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu Glu Lys
 625 630 635 640
 Gly Asp Arg Leu Pro Lys Pro Asp Leu Cys Pro Pro Val Leu Tyr Thr
 645 650 655
 Leu Met Thr Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro Arg Phe
 660 665 670
 Thr Glu Leu Val Cys Ser Leu Ser Asp Val Tyr Gln Met Glu Lys Asp
 675 680 685
 Ile Ala Met Glu Gln Glu Arg Asn Ala Arg Tyr Arg Thr Pro Lys Ile
 690 695 700

Leu Glu Pro Thr Ala Phe Gln Glu Pro Pro Pro Lys Pro Ser Arg Pro
 705 710 715 720
 Lys Tyr Arg Pro Pro Pro Gln Thr Asn Leu Leu Ala Pro Lys Leu Gln
 725 730 735
 Phe Gln Val Pro Glu Gly Leu Cys Ala Ser Ser Pro Thr Leu Thr Ser
 740 745 750
 Pro Met Glu Tyr Pro Ser Pro Val Asn Ser Leu His Thr Pro Pro Leu
 755 760 765
 His Arg His Asn Val Phe Lys Arg His Ser Met Arg Glu Glu Asp Phe
 770 775 780
 Ile Gln Pro Ser Ser Arg Glu Glu Ala Gln Gln Leu Trp Glu Ala Glu
 785 790 795 800
 Lys Val Lys Met Arg Gln Ile Leu Asp Lys Gln Gln Lys Gln Met Val
 805 810 815
 Glu Asp Tyr Gln Trp Leu Arg Gln Glu Glu Lys Ser Leu Asp Pro Met
 820 825 830
 Val Tyr Met Asn Asp Lys Ser Pro Leu Thr Pro Glu Lys Glu Val Gly
 835 840 845
 Tyr Leu Glu Phe Thr Gly Pro Pro Gln Lys Pro Pro Arg Leu Gly Ala
 850 855 860
 Gln Ser Ile Gln Pro Thr Ala Asn Leu Asp Arg Thr Asp Asp Leu Val
 865 870 875 880
 Tyr Leu Asn Val Met Glu Leu Val Arg Ala Val Leu Glu Leu Lys Asn
 885 890 895
 Glu Leu Cys Gln Leu Pro Pro Glu Gly Tyr Val Val Val Lys Asn
 900 905 910
 Val Gly Leu Thr Leu Arg Lys Leu Ile Gly Ser Val Asp Asp Leu Leu
 915 920 925
 Pro Ser Leu Pro Ser Ser Arg Thr Glu Ile Glu Gly Thr Gln Lys
 930 935 940
 Leu Leu Asn Lys Asp Leu Ala Glu Leu Ile Asn Lys Met Arg Leu Ala
 945 950 955 960
 Gln Gln Asn Ala Val Thr Ser Leu Ser Glu Glu Cys Lys Arg Gln Met
 965 970 975
 Leu Thr Ala Ser His Thr Leu Ala Val Asp Ala Lys Asn Leu Leu Asp
 980 985 990
 Ala Val Asp Gln Ala Lys Val Leu Ala Asn Leu Ala His Pro Pro Ala
 995 1000 1005
 Glu

```

<210> 9
<211> 2195
<212> DNA
<213> Homo sapiens

<220>
<223> serine threonine protein kinase casein kinase 2,
      alpha 1 subunit isoform a, transcript variant 2
      (CK2, CK2alpha), CK2 catalytic subunit alpha

<400> 9
agggggagagc ggccgccc gctggcgctt ccaccacagt ttgaagaaaa caggtctgaa 60
acaaggctt acccccagct gcttctgaac acagtgactg ccagatctcc aaacatcaag 120
tccagcttg tccgccaacc tgtctgacat gtcgggaccc gtgccaagca gggccagagt 180
ttacacagat gtaatacac acagacctcg agaatactgg gattacgagt cacatgtgg 240
ggaatggga aatcaagatg actaccagct ggttcgaaaa tttaggcccgg gtaaaatacag 300
tgaagtattt gaagccatca acatcacaaaa taatgaaaaa gtttgttta aaattctcaa 360
gccagtaaaaa aagaagaaaa ttaagcgtga aataaagatt ttggagaatt tgagaggagg 420
tcccaacatc atcacactgg cagacattgt aaaagaccc tgcgtcacgaa ccccccgcct 480
ggttttgaa catgtaaaca acacagactt caagcaattt taccagacgt taacagacta 540
tgatattcga ttttacatgt atgagattct gaaggccctg gattattgtc acagcatggg 600
aattatgcac agagatgtca agccccataa tgtcatgatt gatcatgagc acagaaagct 660
acgactaataa gactgggggt tggctgagtt ttatcatctt ggcacaagaat ataatgtccg 720
agttgcttcc cgataacttca aaggcttgc gctacttgc gactatcaga tgcgtacgat 780
tagtttggat atgtggagtt tgggttgtat gctggcaagt atgatcttc ggaaggagcc 840
atttttccat ggacatgaca attatgatca gttggtgagg atagccaagg ttctggggac 900
agaagattta tatgactata ttgacaaaata caacattgaa tttagatccac gtttcaatga 960
tatcttggc agacactctc gaaagcgtat ggaacgcctt gtcacacgtg aaaatcagca 1020
ccttgcacgc cctgaggccct tggatttccct ggacaaactg ctgcgtatgt accaccagtc 1080
acggcttact gcaagagagg caatggagca ccccttattt tacactgttg tgaaggacca 1140
ggctcgaatg gttcatctca gcatgccagg gggcagtacg cccgtcagca ggcacaaat 1200
gatgtcaggg atttcttcag tgccaaacccc ttccacccctt ggacccctgg caggctcacc 1260
agtgtattgtc gtcgccaacc cccttgggat gcctgttcca gctggcgctg ggcgtcagca 1320
gtaacggccc tatctgtctc ctgatgcctg agcagaggtg ggggagtcca ccctctccct 1380
gatgcagctt ggcctggcg gggaggggtg aaacacttca gaagcaccgt gtcgtacccg 1440
ttgcttggg atttatacgat gttcagtcat aaaaaaaaaa ttataatagg ctgtatccct 1500
tttttctttt ttttttaac tcgaactttt cataactcag gggattccct gaaaaattac 1560
ctgcaggtgg aatatttcat ggacaaaattt tttttctcc cctcccaaat tttagttcctc 1620
atcacaaaag aacaaagata aaccagctc aatcccgct gtcgtatcca ggtggagact 1680
tcttccattt cccaccattt ttccctccacc gtcccacact ttagggggtt ggtatctcg 1740
gctcttctcc agagattaca aaaatgttagc ttctcagggg aggccaggaag aaaggaagga 1800
aggaaagaag gaagggagga cccaatctat aggagcagt gactgcttgc tggctcgtt 1860
catcacatca ctccataagc gttcagtgg gtttatccat gtggctctt gggaaatgt 1920
tcttagttac atcaagatgt tgaaaatcta cccaaaatgc agacagatac taaaacttc 1980
tggtcgttacaa gaatcatgtc ttactgatct aaccctaaat ccaactcatt tatacttt 2040
tttttagttc agttaaaat gttgataaccttccctccctt gtccttacc ttggctttt 2100
ccctgttcat ctcccaacat gtcgtcgtcc atagctggta ggagagggaa ggcacaaatct 2160
ttcttagttt tttttgtttt ggccatccat aattc 2195

```

```
<210> 10
<211> 391
<212> PRT
<213> Homo sapiens

<220>
<223> serine threonine protein kinase casein kinase 2,
      alpha 1 subunit isoform a, transcript variant 2
      (CK2, CK2alpha), CK2 catalytic subunit alpha
```

<400> 10
 Met Ser Gly Pro Val Pro Ser Arg Ala Arg Val Tyr Thr Asp Val Asn
 1 5 10 15

 Thr His Arg Pro Arg Glu Tyr Trp Asp Tyr Glu Ser His Val Val Glu
 20 25 30

 Trp Gly Asn Gln Asp Asp Tyr Gln Leu Val Arg Lys Leu Gly Arg Gly
 35 40 45

 Lys Tyr Ser Glu Val Phe Glu Ala Ile Asn Ile Thr Asn Asn Glu Lys
 50 55 60

 Val Val Val Lys Ile Leu Lys Pro Val Lys Lys Lys Ile Lys Arg
 65 70 75 80

 Glu Ile Lys Ile Leu Glu Asn Leu Arg Gly Gly Pro Asn Ile Ile Thr
 85 90 95

 Leu Ala Asp Ile Val Lys Asp Pro Val Ser Arg Thr Pro Ala Leu Val
 100 105 110

 Phe Glu His Val Asn Asn Thr Asp Phe Lys Gln Leu Tyr Gln Thr Leu
 115 120 125

 Thr Asp Tyr Asp Ile Arg Phe Tyr Met Tyr Glu Ile Leu Lys Ala Leu
 130 135 140

 Asp Tyr Cys His Ser Met Gly Ile Met His Arg Asp Val Lys Pro His
 145 150 155 160

 Asn Val Met Ile Asp His Glu His Arg Lys Leu Arg Leu Ile Asp Trp
 165 170 175

 Gly Leu Ala Glu Phe Tyr His Pro Gly Gln Glu Tyr Asn Val Arg Val
 180 185 190

 Ala Ser Arg Tyr Phe Lys Gly Pro Glu Leu Leu Val Asp Tyr Gln Met
 195 200 205

 Tyr Asp Tyr Ser Leu Asp Met Trp Ser Leu Gly Cys Met Leu Ala Ser
 210 215 220

 Met Ile Phe Arg Lys Glu Pro Phe Phe His Gly His Asp Asn Tyr Asp
 225 230 235 240

 Gln Leu Val Arg Ile Ala Lys Val Leu Gly Thr Glu Asp Leu Tyr Asp
 245 250 255

 Tyr Ile Asp Lys Tyr Asn Ile Glu Leu Asp Pro Arg Phe Asn Asp Ile
 260 265 270

 Leu Gly Arg His Ser Arg Lys Arg Trp Glu Arg Phe Val His Ser Glu
 275 280 285

 Asn Gln His Leu Val Ser Pro Glu Ala Leu Asp Phe Leu Asp Lys Leu
 290 295 300

 Leu Arg Tyr Asp His Gln Ser Arg Leu Thr Ala Arg Glu Ala Met Glu
 305 310 315 320

His	Pro	Tyr	Phe	Tyr	Thr	Val	Val	Lys	Asp	Gln	Ala	Arg	Met	Gly	Ser
						325			330				335		
Ser	Ser	Met	Pro	Gly	Gly	Ser	Thr	Pro	Val	Ser	Ser	Ala	Asn	Met	Met
						340			345			350			
Ser	Gly	Ile	Ser	Ser	Val	Pro	Thr	Pro	Ser	Pro	Leu	Gly	Pro	Leu	Ala
						355			360			365			
Gly	Ser	Pro	Val	Ile	Ala	Ala	Ala	Asn	Pro	Leu	Gly	Met	Pro	Val	Pro
						370			375			380			
Ala	Ala	Ala	Gly	Ala	Gln	Gln									
						385			390						

<210> 11
 <211> 4626
 <212> DNA
 <213> Homo sapiens

<220>
 <223> cMET proto-oncogene tyrosine kinase

<400> 11
 gaattccgccc ctcggccgccc gcggcgcccc gagcgctttg tgagcagatg cggagccgag 60
 tggaggcgcc gagccagatg cggggcgaca gctgacttgc tgagaggagg cggggaggcg 120
 cggagcgccggtgtggctct tgcggcgctg acttctccac tggttcctgg gcaccgaaag 180
 ataaaacctct cataatgaag gcccccgctg tgcttgcacc tggcatcctc gtgctcctgt 240
 ttaccttggt gcagaggagc aatggggagt gtaaagagggc actagcaaag tccgagatga 300
 atgtgaatat gaagtatcag cttcccaact tcaccgcgg aacaccatc cagaatgtca 360
 ttctacatga gcatcacatt ttccttggtg ccactaacta catttatgtt ttaaatgagg 420
 aagacatcca gaagggttgct gagtacaaga ctgggcctgt gctggAACAC ccagattgtt 480
 tcccatgtca ggactgcagc agcaaaagcca attatcagg aggtgttgg aaagataaca 540
 tcaacatggc tctagttgtc gacacctact atgatgatca actcattagc tggcggcagcg 600
 tcaacagagg gacctgcccag cgacatgtct ttcacccacaa tcataactgct gacatacagt 660
 cggaggttca ctgcataattc tccccacaga tagaagagggc cagccagtgt cctgactgtg 720
 tggtgagcgc cctgggagcc aaagtccctt catctgtaaa ggaccgttc atcaacttct 780
 ttgttaggcaa taccataaat tcttcttatt tccagatca tccattgcat tcgatatcag 840
 tgagaaggct aaaggaaacg aaagatgtt ttatgtttt gacggaccag tcctacattg 900
 atgttttacc tgagttcaga gattcttacc ccattaagta tgcctatgcc tttgaaagca 960
 acaattttat ttacttctt acgggtccaaa gggaaactct agatgtcag actttcaca 1020
 caagaataat caggttctgt tccataaact ctggattgca ttccatcatg gaaatgcctc 1080
 tggagtgtat tctcacagaa aagagaaaaa agagatccac aaagaaggaa gtgtttaata 1140
 tacttcaggc tgcgtatgtc agcaagcctg gggcccagct tgctagacaa ataggagcca 1200
 gcctgaatga tgacattctt ttccgggtgt tcgcacaaaag caagccagat tctgcccgaac 1260
 caatggatcg atctgcccattg tgcattcc ctatcaaata tgtcaacgc ttcttcaaca 1320
 agatcgtcaa caaaaacaat gtgagatgtc tccagcattt ttacggaccc aatcatgagc 1380
 actgctttaa taggacactt ctgagaaatt catcaggctg tgaagcgcgc cgtgtatgaat 1440
 atcgaacaga gtttaccaca gctttcagc gcgttgcattt attcatgggt caattcagcg 1500
 aagtccctt aacatctata tccacccatca ttaaaggaga cctcaccata gtaatcttgc 1560
 ggacatcaga gggtcgcttc atgcaggtt tggttctcg atcaggacca tcaacccctc 1620
 atgtgaattt tctcttggac tcccatccag tgcctccaga agtgcattgt gacgatacat 1680
 taaaaccaaaa tggctacaca ctggatcatca ctggaaagaa gatcacaag atcccattga 1740
 atggcttggg ctgcagacat ttccagtcct gcagtcaatg cctctctgccc ccacccttgc 1800
 ttcaatgtgg ctggcgccac gacaaatgtg tgcgtatcgaa ggaatgcctg agcgggacat 1860
 ggactcaaca gatctgtctg cctgcaatct acaagggttt cccaaatagt gcaccccttgc 1920
 aaggagggac aaggctgacc atatgtggct gggactttgg atttcggagg aataataaaat 1980
 ttgatttaaa gaaaactaga gttctccctt gaaatgagag ctgcacccatg actttaagtg 2040
 agagcacatg gaatacattt gaaatgcacag ttggccctgc catgaataag catttcaata 2100
 tgcataat tatttcaat ggccacggga caacacaata cagtcattc tcctatgtgg 2160

atcctgtaat aacaagtatt tcgcccgaat acggccttat ggctgggtgc actttactta 2220
cttaactgg aaattaccta aacagtggga attctagaca catttcaatt ggtggaaaaa 2280
catgtacttt aaaaagtgtg tcaaacagta ttcttgaatg ttataccca gcccaaacc 2340
tttcaactga gtttgcgtt aaattgaaaa ttgacttagc caaccgagag acaagcatct 2400
tcagttaccg tgaagatccc attgtctatg aaattcatcc aaccaaactt ttatttagta 2460
cttgggtggaa agaacacttc aacattgtca gtttctatt ttgcttgcc agtgggtggg 2520
gcacaataac aggtgttggg aaaaacctga atttagttatg tgcccggaga atggtcataa 2580
atgtgcgtga agcaggaagg aactttacag tggcatgtca acatcgctct aattcagaga 2640
taatctgttg taccactcct tccctgcaac agctgaatct gcaactcccc ctgaaaacc 2700
aaggcctttt catgttagat gggatccctt ccaaataactt tgatctcatt tatgtacata 2760
atcctgtgtt taaggcctttt gaaaagccag tgatgtatc aatgggcaat gaaaatgtac 2820
tgaaaattaa gggaaatgtat attgaccctg aaggcgttaa aggtgaagt taaaagttg 2880
gaaataagag ctgtgagaat atacacttac attctgaagc cgtttatgc acggcccc 2940
atgacctgtc gaaatgtaac agcgagctaa atatacgatg gaagcaagca atttctcaa 3000
ccgtccttgg aaaaagtaata gttcaaccag atcagaattt cacaggattt attgctggg 3060
ttgtctcaat atcaacagca ctgttattac tacttgggtt tttctgtgg ctgaaaaaga 3120
gaaagcaaat taaagatctg ggcagtgaat tagttcgcta cgatgcaaga gtacacactc 3180
ctcatttggta taggcttgc ggtggccaa gtgtaaagccc aactacagaa atggtttcaa 3240
atgaatctgt agactaccga gctactttt cagaagatca gtttccataat tcatctcaga 3300
acggttcatg ccgacaagtg cagtatcctc tgacagacat gttcccccattt ctaacttagt 3360
gggactctga tatattccagt ccattactgc aaaatactgt ccacattgac ctcagtgc 3420
taaatccaga gctggccag gcaatgcagc atgtatgtatg tgggcccagt agcctgattt 3480
tgcatttcaa tgaagtcata ggaagagggc attttgggtt tgtatatcat gggactttgt 3540
tgacaaatga tggcaagaaaa attcaactgtg ctgtgaaatc cttgaacaga atcaactgaca 3600
taggagaagt ttcccaattt ctgaccggg gaatcatcat gaaagatttt agtcatcccc 3660
atgtcctctc gctccttggg atctgcctgc gaagtgaagg gtctccgctg gtggcctac 3720
catacatgaa acatggagat ctgcgaaatt tcattcgaaa tgagactcat aatccaactg 3780
taaaagatct tattggcttt ggtctcaag tagccaaagc gatgaaatat cttgcaagca 3840
aaaagttgt ccacagagac ttggctgcaaa gaaactgtat gctggatgaa aaattcacag 3900
tcaagggttgc tgattttggc tttgcccagag acatgtatga taaagaatac tatgtgtac 3960
acaacaaaaac aggtgcaaaag ctgcccagtga agtggatggc tttggaaagt ctgcaactc 4020
aaaagttac caccaagtca gatgtgtgtt ctttggcggt cgccctctgg gagctgtatg 4080
caagaggagc cccacccctt cctgacgtaa acaccccttga tataactgtt tacttggc 4140
aagggagaag actcctacaa cccgaaatact gcccagaccc ctttatgaa gtaatgctaa 4200
aatgctggca ccctaaagcc gaaatgcgcc catccttttc tgaacttggc tcccgatata 4260
cagcgatctt ctctactttc attggggagc actatgtcca tgtgaacgct acttatgtga 4320
acgtaaaatg tgcgtccg tattttctc ttttgtcattc agaagataac gctgtatgat 4380
aggtggacac acgaccagcc tccttctggg agacatcata gtgttagtac tatgtcaag 4440
caacagtcca cactttgtcc aatggtttt tcactgcctg acctttaaaa ggcctcgat 4500
attctttgtc ctttgcata ggacttgtat tttttttttt attactggat tctaaggaat 4560
tttttatctg acagagcatc agaaccagag gcttggccc acaggccagg gaccaatgc 4620
ctgcag 4626

<210> 12
<211> 1408
<212> PRT
<213> Homo sapiens

<220>
<223> cMET proto-oncogene tyrosine kinase

<400> 12
Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu Phe
1 5 10 15

Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
20 25 30

Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
35 40 45

Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
 50 55 60

Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
 65 70 75 80

Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
 85 90 95

Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
 100 105 110

Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr Tyr Tyr Asp Asp
 115 120 125

Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr Cys Gln Arg His
 130 135 140

Val Phe Pro His Asn His Thr Ala Asp Ile Gln Ser Glu Val His Cys
 145 150 155 160

Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val
 165 170 175

Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe
 180 185 190

Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp
 195 200 205

His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp
 210 215 220

Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu
 225 230 235 240

Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn
 245 250 255

Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln
 260 265 270

Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu
 275 280 285

His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg
 290 295 300

Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala
 305 310 315 320

Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
 325 330 335

Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp
 340 345 350

Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
 355 360 365

Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg
 370 375 380
 Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
 385 390 395 400
 Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
 405 410 415
 Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
 420 425 430
 Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
 435 440 445
 Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
 450 455 460
 Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
 465 470 475 480
 Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
 485 490 495
 Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys
 500 505 510
 Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln Ser Cys Ser Gln
 515 520 525
 Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
 530 535 540
 Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
 545 550 555 560
 Cys Leu Pro Ala Ile Tyr Lys Val Phe Pro Asn Ser Ala Pro Leu Glu
 565 570 575
 Gly Gly Thr Arg Leu Thr Ile Cys Gly Trp Asp Phe Gly Phe Arg Arg
 580 585 590
 Asn Asn Lys Phe Asp Leu Lys Lys Thr Arg Val Leu Leu Gly Asn Glu
 595 600 605
 Ser Cys Thr Leu Thr Leu Ser Glu Ser Thr Met Asn Thr Leu Lys Cys
 610 615 620
 Thr Val Gly Pro Ala Met Asn Lys His Phe Asn Met Ser Ile Ile Ile
 625 630 635 640
 Ser Asn Gly His Gly Thr Thr Gln Tyr Ser Thr Phe Ser Tyr Val Asp
 645 650 655
 Pro Val Ile Thr Ser Ile Ser Pro Lys Tyr Gly Pro Met Ala Gly Gly
 660 665 670
 Thr Leu Leu Thr Leu Thr Gly Asn Tyr Leu Asn Ser Gly Asn Ser Arg
 675 680 685

His	Ile	Ser	Ile	Gly	Gly	Lys	Thr	Cys	Thr	Leu	Lys	Ser	Val	Ser	Asn
690															
															700
Ser	Ile	Leu	Glu	Cys	Tyr	Thr	Pro	Ala	Gln	Thr	Ile	Ser	Thr	Glu	Phe
705															720
Ala	Val	Lys	Leu	Lys	Ile	Asp	Leu	Ala	Asn	Arg	Glu	Thr	Ser	Ile	Phe
															735
Ser	Tyr	Arg	Glu	Asp	Pro	Ile	Val	Tyr	Glu	Ile	His	Pro	Thr	Lys	Ser
															750
Phe	Ile	Ser	Thr	Trp	Trp	Lys	Glu	Pro	Leu	Asn	Ile	Val	Ser	Phe	Leu
755															
															765
Phe	Cys	Phe	Ala	Ser	Gly	Gly	Ser	Thr	Ile	Thr	Gly	Val	Gly	Lys	Asn
															780
Leu	Asn	Ser	Val	Ser	Val	Pro	Arg	Met	Val	Ile	Asn	Val	His	Glu	Ala
785															800
Gly	Arg	Asn	Phe	Thr	Val	Ala	Cys	Gln	His	Arg	Ser	Asn	Ser	Glu	Ile
															815
Ile	Cys	Cys	Thr	Thr	Pro	Ser	Leu	Gln	Gln	Leu	Asn	Leu	Gln	Leu	Pro
															830
Leu	Lys	Thr	Lys	Ala	Phe	Phe	Met	Leu	Asp	Gly	Ile	Leu	Ser	Lys	Tyr
															845
Phe	Asp	Leu	Ile	Tyr	Val	His	Asn	Pro	Val	Phe	Lys	Pro	Phe	Glu	Lys
850															860
Pro	Val	Met	Ile	Ser	Met	Gly	Asn	Glu	Asn	Val	Leu	Glu	Ile	Lys	Gly
865															880
Asn	Asp	Ile	Asp	Pro	Glu	Ala	Val	Lys	Gly	Glu	Val	Leu	Lys	Val	Gly
															895
Asn	Lys	Ser	Cys	Glu	Asn	Ile	His	Leu	His	Ser	Glu	Ala	Val	Leu	Cys
															910
Thr	Val	Pro	Asn	Asp	Leu	Leu	Lys	Leu	Asn	Ser	Glu	Leu	Asn	Ile	Glu
															925
Trp	Lys	Gln	Ala	Ile	Ser	Ser	Thr	Val	Leu	Gly	Lys	Val	Ile	Val	Gln
															940
Pro	Asp	Gln	Asn	Phe	Thr	Gly	Leu	Ile	Ala	Gly	Val	Val	Ser	Ile	Ser
945															960
Thr	Ala	Leu	Leu	Leu	Leu	Gly	Phe	Phe	Leu	Trp	Leu	Lys	Lys	Arg	
															975
Lys	Gln	Ile	Lys	Asp	Leu	Gly	Ser	Glu	Leu	Val	Arg	Tyr	Asp	Ala	Arg
															990
Val	His	Thr	Pro	His	Leu	Asp	Arg	Leu	Val	Ser	Ala	Arg	Ser	Val	Ser
															1005

Pro Thr Thr Glu Met Val Ser Asn Glu Ser Val Asp Tyr Arg Ala Thr
 1010 1015 1020

 Phe Pro Glu Asp Gln Phe Pro Asn Ser Ser Gln Asn Gly Ser Cys Arg
 1025 1030 1035 1040

 Gln Val Gln Tyr Pro Leu Thr Asp Met Ser Pro Ile Leu Thr Ser Gly
 1045 1050 1055

 Asp Ser Asp Ile Ser Ser Pro Leu Leu Gln Asn Thr Val His Ile Asp
 1060 1065 1070

 Leu Ser Ala Leu Asn Pro Glu Leu Val Gln Ala Val Gln His Val Val
 1075 1080 1085

 Ile Gly Pro Ser Ser Leu Ile Val His Phe Asn Glu Val Ile Gly Arg
 1090 1095 1100

 Gly His Phe Gly Cys Val Tyr His Gly Thr Leu Leu Asp Asn Asp Gly
 1105 1110 1115 1120

 Lys Lys Ile His Cys Ala Val Lys Ser Leu Asn Arg Ile Thr Asp Ile
 1125 1130 1135

 Gly Glu Val Ser Gln Phe Leu Thr Glu Gly Ile Ile Met Lys Asp Phe
 1140 1145 1150

 Ser His Pro Asn Val Leu Ser Leu Leu Gly Ile Cys Leu Arg Ser Glu
 1155 1160 1165

 Gly Ser Pro Leu Val Val Leu Pro Tyr Met Lys His Gly Asp Leu Arg
 1170 1175 1180

 Asn Phe Ile Arg Asn Glu Thr His Asn Pro Thr Val Lys Asp Leu Ile
 1185 1190 1195 1200

 Gly Phe Gly Leu Gln Val Ala Lys Ala Met Lys Tyr Leu Ala Ser Lys
 1205 1210 1215

 Lys Phe Val His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Asp Glu
 1220 1225 1230

 Lys Phe Thr Val Lys Val Ala Asp Phe Gly Leu Ala Arg Asp Met Tyr
 1235 1240 1245

 Asp Lys Glu Tyr Tyr Ser Val His Asn Lys Thr Gly Ala Lys Leu Pro
 1250 1255 1260

 Val Lys Trp Met Ala Leu Glu Ser Leu Gln Thr Gln Lys Phe Thr Thr
 1265 1270 1275 1280

 Lys Ser Asp Val Trp Ser Phe Gly Val Val Leu Trp Glu Leu Met Thr
 1285 1290 1295

 Arg Gly Ala Pro Pro Tyr Pro Asp Val Asn Thr Phe Asp Ile Thr Val
 1300 1305 1310

 Tyr Leu Leu Gln Gly Arg Arg Leu Leu Gln Pro Glu Tyr Cys Pro Asp
 1315 1320 1325

Pro Leu Tyr Glu Val Met Leu Lys Cys Trp His Pro Lys Ala Glu Met
1330 1335 1340

Arg Pro Ser Phe Ser Glu Leu Val Ser Arg Ile Ser Ala Ile Phe Ser
1345 1350 1355 1360

Thr Phe Ile Gly Glu His Tyr Val His Val Asn Ala Thr Tyr Val Asn
1365 1370 1375

Val Lys Cys Val Ala Pro Tyr Pro Ser Leu Leu Ser Ser Glu Asp Asn
1380 1385 1390

Ala Asp Asp Glu Val Asp Thr Arg Pro Ala Ser Phe Trp Glu Thr Ser
1395 1400 1405

<210> 13

<211> 3350

<212> DNA

<213> Homo sapiens

<220>

<223> flap structure-specific endonuclease 1 (FEN1)
5'-3' exonuclease

<400> 13

cacagtccac tctgtcaggg tttaaggcag gaaaaacatg ctcatttga tggtaatatt 60
cttccttctc aacattccat ttctcctggc aaatttcatg gatcccagat gcttttggaa 120
aataaaatttgc aatgaaaatca aggatgaagt ccttgggatg acttgttctc tcattcatttgc 180
aacagttcag aagactatgg acaaagatta ttcaaccag actctgaatg tcctaaatc 240
aactacaaac cacaatatg ccttggcatt ggcctttaca gtggatgaaa tcaacaggaa 300
tcctgatctt ttaccaaata tgcgtctgtat tataaaatc aatttgggtc attgtatgg 360
aaaaactgtt acaactctat ccgatttatt taatccaaat aatcatctcc atttccccaa 420
ttattttatgt aatgaaggga ttatgtgttt gggtctgtttt acaggaccac attggagagc 480
atctttatct ctctggatat ccgtgtatgt ctacctgtct ccacatttcc ttcatgtttc 540
ctatggacct ttctactcca tcttcagtga taatgaacaa tattcatttcc tctatcagat 600
gggccccaaag gactcatcac tagcatttgc aatgggtctcc ttccataattt acttcaagtg 660
gaactgggtt gggctatttta tctcagatga tgcataaggc aatcaatttcc tctcagagtt 720
gaaaaaaagag agccaaacca aggatatttgc ctttgcctt gtgaacatga tatcagtcag 780
tgatgtttca tactatcata aaactgaaat gtactacaac caaatttgc tgcgtatccac 840
aaagggttatt atcattttatg gggaaacaaa cagtttatttta gaatttgc tcaaatgtg 900
gtcatctcca gttaaacaga gaatatgggt caccacaaaa caatttgcattt gcccattacc 960
taagagagac ttaactcatg gcacatttca tggaccctt acatttctac accactatgg 1020
tgagattttctt ggctttaaaa attttgcata gacacggatc aatctcagaa gcacagattt 1080
atatcttagta atgcccagatg gggaaatatttta taactatgaa gcctcagcat ctaactgtaa 1140
aataactgaga aactatttat ccaatatctc actggaaatgg ctaatggaaac agaaatttgc 1200
catgtcattt agtgattata gtcacaaatc atacaatgtt gtatatgcca ttgctcatgc 1260
actccatgag aagaatctgc aagaaggatgaa aaatcaggca ataaacaatg cgaaaggaga 1320
aaataactcac tgcttgcatttca taaacttatttca tctgagaatgg acccacttca ctaatttctc 1380
tggaaacaga gtaattatgaa aacagagaga agtagtgcatttgc gggactata atattgttca 1440
catgtgaaat ttctcacaac gccttggat taaggtgaaatggacatgc tcatgttctt 1500
ttttccacag ggtcaacagt tacacttata tgcgtatgcacttgc gttttctgttgc 1560
tagaaagatg ccatttcatttca tgcgtatgcacttgc agatttgcatttgc gttttctgttgc 1620
gaaggaggaa atggcagcct gctgtttgtt ttgcacccat tgcctgaaa atgaaatttgc 1680
taatgagacg atgggtgtat tttgggtctt cgtgaaggacatgc tcatgttctt 1740
ggccaataac agaatttcatttca gctacatttca aatcgatgc tcatgttctt 1800
ctccttttc ttcatttgcatttca tgcgtatgcacttgc agatttgcatttgc gttttctgttgc 1860
tggaaatcttc tttactgtgg ctatttccat agtttgcatttgc aatcgatgc tcatgttctt 1920
ggcttcaaa gtcacagacc caggaagaca attaagaatc tttttggat tggggacacc 1980
caactacatttcaatttca ttcatttgcatttca gcaatgttatttgc tgcgtatgc tcatgttctt 2040
agtttcttcctt cccttgcatttca tgcgtatgcacttgc agatttgcatttgc gttttctgttgc 2100

gtgcaacaag	ggctccatta	ctgcattcta	ctgtgtcctg	ggatacttgg	cctgcctggc	2160
ctttggaagc	ttcaactatag	ctttcttggc	aaagaacctg	cctgacacat	tcaacagaagc	2220
caagttcttg	accctcagca	tgcttagtgtt	ctgcgtgtc	tggttcacct	tcctccctgt	2280
ctaccatagc	accaaggcga	aggcatggt	tgctgtggag	atcttctcca	tcttggcattc	2340
tagtgcaggg	atgctggat	gcattttgc	acccaaagtt	tacatcattt	taatgagacc	2400
agacagaaaat	tcgatccaca	aaatcaggga	gaaatcatat	ttctgaaaag	gtatttcagg	2460
aattctgtca	aatgtaaaagt	tgatacatac	accccaaata	tttagttaca	gagcatatat	2520
ctagtttag	aatcaacttc	actggttcct	ctagttaaagc	atagaagttac	catatgtact	2580
gatcttgcatt	atgttgcata	taaaatctta	caatcatcata	tttgcttagt	atcttctgga	2640
agaagtaaaa	ttttcaaaata	actagtacaa	ttttatttcat	tattttgctt	tcatgaggat	2700
ttccccctgg	taacttcaaa	taaattttat	aagtcaagttg	aatatataac	cttacataga	2760
aagtgagttc	taggacagac	agggattata	catagaaaca	aactaactaa	aatcaacaa	2820
agatgaaatc	agaacacatt	ttcttatttc	cagtaggaac	acatacttga	cagaatactg	2880
tcttttttgc	agctgcttt	taagatattg	gccaaatagtc	taagctgaaa	atgttcttta	2940
tctactctca	aatacaaaaaaaa	tattatatcc	aacaatggac	agaatctgag	aactcctgtg	3000
gtttaggttag	ggaatagttt	gaagatactg	agaaggaggt	gaccctatgg	aatacaaagc	3060
agtctcaact	aacctggaca	accaagggtcc	ctcagacact	gagccactaa	caagtcagcc	3120
tactccagct	gttatgagggc	ccccaaaaca	tatgcaacat	aggattgcct	ggtccagcct	3180
cagcaagaga	atacacaccc	aaccacagag	agacttcccc	aagggtattgg	ggaggtctgg	3240
ggtttggaga	gttgccgatt	gtcccttgat	gatttggaaagg	aggtatttgg	tgagaatgaa	3300
tcagggggaa	gacttaggaag	gggataatga	tggaaactgtt	aaaaaaaaaaa		3350

```
<210> 14
<211> 380
<212> PRT
<213> Homo sapiens
```

<220>
<223> flap structure-specific endonuclease 1 (FEN1)
5'-3' exonuclease

<400> 14
Met Gly Ile Gln Gly Leu Ala Lys Leu Ile Ala Asp Val Ala Pro Ser
1 5 10 15

Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
20 25 30

Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
35 40 45

Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
 50 55 60

Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
65 70 75 80

Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu
85 90 95

Leu Ala Lys Arg Ser Glu Arg Arg Ala Glu Ala Glu Lys Gln Leu Gln
100 105 110

Gln Ala Gln Ala Ala Gly Ala Glu Gln Glu Val Glu Lys Phe Thr Lys
 115 120 125

Arg Leu Val Lys Val Thr Lys Gln His Asn Asp Glu Cys Lys His Leu
130 135 140

Leu Ser Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu
 145 150 155 160
 Ala Ser Cys Ala Ala Leu Val Lys Ala Gly Lys Val Tyr Ala Ala Ala
 165 170 175
 Thr Glu Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg
 180 185 190
 His Leu Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His
 195 200 205
 Leu Ser Arg Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val
 210 215 220
 Asp Leu Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly
 225 230 235 240
 Ile Gly Pro Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys Ser Ile
 245 250 255
 Glu Glu Ile Val Arg Arg Leu Asp Pro Asn Lys Tyr Pro Val Pro Glu
 260 265 270
 Asn Trp Leu His Lys Glu Ala His Gln Leu Phe Leu Glu Pro Glu Val
 275 280 285
 Leu Asp Pro Glu Ser Val Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu
 290 295 300
 Glu Leu Ile Lys Phe Met Cys Gly Glu Lys Gln Phe Ser Glu Glu Arg
 305 310 315 320
 Ile Arg Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr
 325 330 335
 Gln Gly Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser
 340 345 350
 Ala Lys Arg Lys Glu Pro Glu Pro Lys Gly Ser Thr Lys Lys Ala
 355 360 365
 Lys Thr Gly Ala Ala Gly Lys Phe Lys Arg Gly Lys
 370 375 380

<210> 15
 <211> 4276
 <212> DNA
 <213> Homo sapiens

<220>
 <223> REV1 dCMP transferase

<400> 15
 agagccacccg cggagcgcgc gcgggggttgg ttgccgcgag cgtgggggag cgtggaccgc 60
 ggcgcgtgctc agcgggtgggg ctgccttccc ccggccctcc tccctggtcc ctggcgaggg 120
 cactggcggc ggcggggccg gggtccgcaa ggcggagaa ggccgcccggg cccgggcatg 180
 gtgggtctggg gcaacgcgga agaagctcca ccatgaggcg aggtggatgg aggaagcag 240
 ctgaaaatgta tggctggaa acatgggtg ggtatatggc tgccaaggtc cagaaattgg 300
 aggaacagtt tcgatcagat gctgctatgc agaaggatgg gacttcatct acaattttta 360

gtggagttgc catctatgtt aatggataca cagatccttc cgctgaggaa ttgagaaaaac 420
 taatgatgtt gcatggaggt caataccatg tatattattc cagatctaaa acaacacata 480
 ttattgccac aaatctccc aatgcaaaaa ttaaagaatt aaaggggaa aaagtaattc 540
 gaccagaatg gattgtggaa agcatcaaag ctggacgact cctctcctac attccatatc 600
 agctgtcac acagcagtcc agtgtcaga aaggtcttag ctttaatcct gtatgcagac 660
 ctgaggatcc tctgccaggt ccaagcaata tagccaaaca gctcaacaac agggtaaattc 720
 acatcgtaa gaagattgaa acggaaaatg aagtcaaagt caatggcatg aacagttgaa 780
 atgaagaaga tgaaaataat gattttagt ttgtggatct ggagcagacc tctccggaa 840
 gaaaaacagaa tggaaattccg catcccagag ggagcactgc catttttaat ggacacactc 900
 cttagctcaa tgggcctta aagacacagg attgcttggt gcccattggc aacagttgtt 960
 ccagcaggct ttctccagcc ttttcccagg aggaggataa ggctgagaag agcagcactg 1020
 atttcagaga ctgcactctg cagcgttgc agcaaagcac cagaaacaca gatgctttgc 1080
 ggaatccaca cagaataat tctttctcat tattcacctt gcacagtaac actaaaatca 1140
 atgggtctca ccactccact gttcaggggc cttcaagcac aaaaagcaact tcttcagtt 1200
 ctacgtttag caaggcagca ctttcagttgc catccaaacc ttcagactgc aatttttattt 1260
 caaaattctca ttctcattca agactgcattt acatataat gtggaagtgtt gaatttgactg 1320
 agtttgtcaa taccctacaa agacaaagta atggtatctt tccaggaagg gaaaagttaa 1380
 aaaaaatgaa aacaggcagg tctgcacttg ttgttaactga cacaggagat atgtcagtt 1440
 tgaattctcc cagacatcg agctgtataa tgcattgttga tatggattgc ttctttgtat 1500
 cagtgggtat acgaaataga ccagatctca aaggaaaacc agtggctgtt acaagtaaca 1560
 gaggcacagg aagggcacct ttacgtctg gcgctaacc ccagctggag tggcagtatt 1620
 accagaataa aatctgaaa ggcaaagcag cagatatacc agattcatca ttgtgggaga 1680
 atccagattc tgcgcaagca aatggattt attctgtttt gtcaaggggct gaaatttgcatt 1740
 cttagttagtta tgaggccagg caacttggca ttaagaacgg aatgtttttt gggcatgcta 1800
 aacaactatg tcctaattctt caagctttc catacgattt tcatgcataat aaggaagtctg 1860
 cacaacatt gtatgaaaca ttggcaagct acactataa cattgaagct gtcagttgtt 1920
 atgaagcgct ggttagacattt accgaaatcc ttgcagagac caaacttact cctgtatgaat 1980
 ttgcaatgc tgttcgtatg gaaatcaaag accagacgaa atgtgtgttgc tctgttggaa 2040
 ttggttctaa tattctcctg gctagaatgg caactagaaa agcaaaacca gatgggcagt 2100
 accacctaaa accagaagaa gtagatgatt ttatcagagg ccagcttagt accaatctac 2160
 caggagttgg acattcaatg gaatctaagt tggcatctt gggattaaaa acttgtggag 2220
 acttgcagta tatgaccatg gcaaaaactcc aaaaagaatt tggtccaaa acaggtcaga 2280
 tgctttatag gttctgcccgt ggcttggatg atagaccagt tcgaactgaa aaggaaagaa 2340
 aatctgtttc agctgagatc aactatgaa taaggtttac tcagccaaaa gaggcagaag 2400
 cttttcttct gagtcttca gaagaaattt aaagaagact agaagccact ggcattgaagg 2460
 gtaaacgtct aactctaaa atcatggtac gaaagcctgg ggctctgtt gaaactgcaa 2520
 aatttggagg ccatggaatt tggataaca ttgccaggac tggtaactt gaccaggcaa 2580
 cagataatgc aaaaataatt ggaaaggcga tgctaaacat gtttcataca atgaaactaa 2640
 atatatcaga tatgagaggg gttgggattt acgtgaatca gttggttcca actaatctga 2700
 acccttccac atgtcccagt cggccatcag ttctgtcaag ccactttctt agtgggtcat 2760
 actctgtccg tgatgtcttca caagttcaga aagctaagaa atccaccgaa gaggagcaca 2820
 aagaagtatt tcgggctgtt gtggatctgg aaatatcatc tgcttctaga acttgcactt 2880
 tcttgccacc ttttctgtca catctgccga ccagtcctga tactaacaag gctgagttt 2940
 cagggaaatg gaatggtcta catactcctg tcagtgtgca gtcgagactt aacctgagta 3000
 tagaggtccc gtcaccttcc cagctggatc agtctgtttt agaagcactt ccacctgatc 3060
 tccgggaaaca agtagagcaa gtctgtgttccagcaagc agagtcacat gggcacaaaaa 3120
 agaaaagaacc agtaaatggc tggtaatacag gaattttgccc acaaccagtt gggacagtt 3180
 tggtaaat accagaaccc caagaatcga acagtgcacgc aggaataaaat ttaatagccc 3240
 ttccagcatt ttcacaggtt gaccctgagg tatttgcattt ctttcctgtt gaaacttcaga 3300
 gggagctgaa agcagcgtat gatcaaagac aaaggcaggcg cggaaacacgc actcaccaggc 3360
 agtcagccag cgcattctgtt ccaaagaatc ctttacttca tctaaaggca gcaagtggaaag 3420
 aaaaagaaaag aaacaagaag aaaaaaaacca ttgtttcacc aaaaaggatt cagagtccct 3480
 tgaataacaa gctgtttaac agtctgttca aaactctgttcc agggccctgtt ggcagttcccc 3540
 agaagttaat tgatgggttt cttaaacatg aaggaccttcc tgcagagaaaa cccctggaaag 3600
 aactctctgc ttctacttca ggtgtccag gcctttcttag tttgcatttgc gaccctgatc 3660
 gctgtgttag acctccagca cccaaatcttag ctggagctgt tggtaatttcaat gatgtgaaga 3720
 ctttgctcag agaatggata actacaattt cagatccaat ggaagaagac attctccaaag 3780
 ttgtgaaataa ctgtactgtt ctaatagaag aaaaagattt gggaaaactg gatctgtt 3840
 taaaatacat gaaaaggctg atgcagcaat cggtggaaatc ggtttggaaat atggcattt 3900
 actttattct tgacaatgtc caggtggttt tacaacaaac ttatggaaagc acattaaaag 3960
 ttacataaaat attaccagag agcctgtatgc tctctgtatgc ctgtggccata agtgcattgtt 4020

aggtatttgc aaagtgcatg atagtaatgc tcggagttt tataattta aatttcttt 4080
aaagcaagtg ttttgacat ttctttcaa aaagtgccaa atttgcagt attgcata 4140
aataattgtg ttaattattt tactgttagca tagattctat ttacaaaatg tttgtttata 4200
aagttttatg gattttaca gtgaagtgtt tacagttgtt taataaagaa ctgtatgtaa 4260
aaaaaaaaaaa aaaaaaa 4276

<210> 16
<211> 1251
<212> PRT
<213> Homo sapiens

<220>
<223> REV1 dCMP transferase

<400> 16
Met Arg Arg Gly Gly Trp Arg Lys Arg Ala Glu Asn Asp Gly Trp Glu
1 5 10 15

Thr Trp Gly Gly Tyr Met Ala Ala Lys Val Gln Lys Leu Glu Glu Gln
20 25 30

Phe Arg Ser Asp Ala Ala Met Gln Lys Asp Gly Thr Ser Ser Thr Ile
35 40 45

Phe Ser Gly Val Ala Ile Tyr Val Asn Gly Tyr Thr Asp Pro Ser Ala
50 55 60

Glu Glu Leu Arg Lys Leu Met Met Leu His Gly Gly Gln Tyr His Val
65 70 75 80

Tyr Tyr Ser Arg Ser Lys Thr Thr His Ile Ile Ala Thr Asn Leu Pro
85 90 95

Asn Ala Lys Ile Lys Glu Leu Lys Gly Glu Lys Val Ile Arg Pro Glu
100 105 110

Trp Ile Val Glu Ser Ile Lys Ala Gly Arg Leu Leu Ser Tyr Ile Pro
115 120 125

Tyr Gln Leu Tyr Thr Lys Gln Ser Ser Val Gln Lys Gly Leu Ser Phe
130 135 140

Asn Pro Val Cys Arg Pro Glu Asp Pro Leu Pro Gly Pro Ser Asn Ile
145 150 155 160

Ala Lys Gln Leu Asn Asn Arg Val Asn His Ile Val Lys Lys Ile Glu
165 170 175

Thr Glu Asn Glu Val Lys Val Asn Gly Met Asn Ser Trp Asn Glu Glu
180 185 190

Asp Glu Asn Asn Asp Phe Ser Phe Val Asp Leu Glu Gln Thr Ser Pro
195 200 205

Gly Arg Lys Gln Asn Gly Ile Pro His Pro Arg Gly Ser Thr Ala Ile
210 215 220

Phe Asn Gly His Thr Pro Ser Ser Asn Gly Ala Leu Lys Thr Gln Asp
225 230 235 240

Cys Leu Val Pro Met Val Asn Ser Val Ala Ser Arg Leu Ser Pro Ala
 245 250 255
 Phe Ser Gln Glu Glu Asp Lys Ala Glu Lys Ser Ser Thr Asp Phe Arg
 260 265 270
 Asp Cys Thr Leu Gln Gln Leu Gln Gln Ser Thr Arg Asn Thr Asp Ala
 275 280 285
 Leu Arg Asn Pro His Arg Thr Asn Ser Phe Ser Leu Ser Pro Leu His
 290 295 300
 Ser Asn Thr Lys Ile Asn Gly Ala His His Ser Thr Val Gln Gly Pro
 305 310 315 320
 Ser Ser Thr Lys Ser Thr Ser Val Ser Thr Phe Ser Lys Ala Ala
 325 330 335
 Pro Ser Val Pro Ser Lys Pro Ser Asp Cys Asn Phe Ile Ser Asn Phe
 340 345 350
 Tyr Ser His Ser Arg Leu His His Ile Ser Met Trp Lys Cys Glu Leu
 355 360 365
 Thr Glu Phe Val Asn Thr Leu Gln Arg Gln Ser Asn Gly Ile Phe Pro
 370 375 380
 Gly Arg Glu Lys Leu Lys Lys Met Lys Thr Gly Arg Ser Ala Leu Val
 385 390 395 400
 Val Thr Asp Thr Gly Asp Met Ser Val Leu Asn Ser Pro Arg His Gln
 405 410 415
 Ser Cys Ile Met His Val Asp Met Asp Cys Phe Phe Val Ser Val Gly
 420 425 430
 Ile Arg Asn Arg Pro Asp Leu Lys Gly Lys Pro Val Ala Val Thr Ser
 435 440 445
 Asn Arg Gly Thr Gly Arg Ala Pro Leu Arg Pro Gly Ala Asn Pro Gln
 450 455 460
 Leu Glu Trp Gln Tyr Tyr Gln Asn Lys Ile Leu Lys Gly Lys Ala Ala
 465 470 475 480
 Asp Ile Pro Asp Ser Ser Leu Trp Glu Asn Pro Asp Ser Ala Gln Ala
 485 490 495
 Asn Gly Ile Asp Ser Val Leu Ser Arg Ala Glu Ile Ala Ser Cys Ser
 500 505 510
 Tyr Glu Ala Arg Gln Leu Gly Ile Lys Asn Gly Met Phe Phe Gly His
 515 520 525
 Ala Lys Gln Leu Cys Pro Asn Leu Gln Ala Val Pro Tyr Asp Phe His
 530 535 540
 Ala Tyr Lys Glu Val Ala Gln Thr Leu Tyr Glu Thr Leu Ala Ser Tyr
 545 550 555 560

Thr His Asn Ile Glu Ala Val Ser Cys Asp Glu Ala Leu Val Asp Ile
 565 570 575
 Thr Glu Ile Leu Ala Glu Thr Lys Leu Thr Pro Asp Glu Phe Ala Asn
 580 585 590
 Ala Val Arg Met Glu Ile Lys Asp Gln Thr Lys Cys Ala Ala Ser Val
 595 600 605
 Gly Ile Gly Ser Asn Ile Leu Leu Ala Arg Met Ala Thr Arg Lys Ala
 610 615 620
 Lys Pro Asp Gly Gln Tyr His Leu Lys Pro Glu Glu Val Asp Asp Phe
 625 630 635 640
 Ile Arg Gly Gln Leu Val Thr Asn Leu Pro Gly Val Gly His Ser Met
 645 650 655
 Glu Ser Lys Leu Ala Ser Leu Gly Ile Lys Thr Cys Gly Asp Leu Gln
 660 665 670
 Tyr Met Thr Met Ala Lys Leu Gln Lys Glu Phe Gly Pro Lys Thr Gly
 675 680 685
 Gln Met Leu Tyr Arg Phe Cys Arg Gly Leu Asp Asp Arg Pro Val Arg
 690 695 700
 Thr Glu Lys Glu Arg Lys Ser Val Ser Ala Glu Ile Asn Tyr Gly Ile
 705 710 715 720
 Arg Phe Thr Gln Pro Lys Glu Ala Glu Ala Phe Leu Leu Ser Leu Ser
 725 730 735
 Glu Glu Ile Gln Arg Arg Leu Glu Ala Thr Gly Met Lys Gly Lys Arg
 740 745 750
 Leu Thr Leu Lys Ile Met Val Arg Lys Pro Gly Ala Pro Val Glu Thr
 755 760 765
 Ala Lys Phe Gly Gly His Gly Ile Cys Asp Asn Ile Ala Arg Thr Val
 770 775 780
 Thr Leu Asp Gln Ala Thr Asp Asn Ala Lys Ile Ile Gly Lys Ala Met
 785 790 795 800
 Leu Asn Met Phe His Thr Met Lys Leu Asn Ile Ser Asp Met Arg Gly
 805 810 815
 Val Gly Ile His Val Asn Gln Leu Val Pro Thr Asn Leu Asn Pro Ser
 820 825 830
 Thr Cys Pro Ser Arg Pro Ser Val Gln Ser Ser His Phe Pro Ser Gly
 835 840 845
 Ser Tyr Ser Val Arg Asp Val Phe Gln Val Gln Lys Ala Lys Lys Ser
 850 855 860
 Thr Glu Glu Glu His Lys Glu Val Phe Arg Ala Ala Val Asp Leu Glu
 865 870 875 880

Ile Ser Ser Ala Ser Arg Thr Cys Thr Phe Leu Pro Pro Phe Pro Ala
 885 890 895
 His Leu Pro Thr Ser Pro Asp Thr Asn Lys Ala Glu Ser Ser Gly Lys
 900 905 910
 Trp Asn Gly Leu His Thr Pro Val Ser Val Gln Ser Arg Leu Asn Leu
 915 920 925
 Ser Ile Glu Val Pro Ser Pro Ser Gln Leu Asp Gln Ser Val Leu Glu
 930 935 940
 Ala Leu Pro Pro Asp Leu Arg Glu Gln Val Glu Gln Val Cys Ala Val
 945 950 955 960
 Gln Gln Ala Glu Ser His Gly Asp Lys Lys Lys Glu Pro Val Asn Gly
 965 970 975
 Cys Asn Thr Gly Ile Leu Pro Gln Pro Val Gly Thr Val Leu Leu Gln
 980 985 990
 Ile Pro Glu Pro Gln Glu Ser Asn Ser Asp Ala Gly Ile Asn Leu Ile
 995 1000 1005
 Ala Leu Pro Ala Phe Ser Gln Val Asp Pro Glu Val Phe Ala Ala Leu
 1010 1015 1020
 Pro Ala Glu Leu Gln Arg Glu Leu Lys Ala Ala Tyr Asp Gln Arg Gln
 1025 1030 1035 1040
 Arg Gln Gly Glu Asn Ser Thr His Gln Gln Ser Ala Ser Ala Ser Val
 1045 1050 1055
 Pro Lys Asn Pro Leu Leu His Leu Lys Ala Ala Val Lys Glu Lys Lys
 1060 1065 1070
 Arg Asn Lys Lys Lys Lys Thr Ile Gly Ser Pro Lys Arg Ile Gln Ser
 1075 1080 1085
 Pro Leu Asn Asn Lys Leu Leu Asn Ser Pro Ala Lys Thr Leu Pro Gly
 1090 1095 1100
 Ala Cys Gly Ser Pro Gln Lys Leu Ile Asp Gly Phe Leu Lys His Glu
 1105 1110 1115 1120
 Gly Pro Pro Ala Glu Lys Pro Leu Glu Leu Ser Ala Ser Thr Ser
 1125 1130 1135
 Gly Val Pro Gly Leu Ser Ser Leu Gln Ser Asp Pro Ala Gly Cys Val
 1140 1145 1150
 Arg Pro Pro Ala Pro Asn Leu Ala Gly Ala Val Glu Phe Asn Asp Val
 1155 1160 1165
 Lys Thr Leu Leu Arg Glu Trp Ile Thr Thr Ile Ser Asp Pro Met Glu
 1170 1175 1180
 Glu Asp Ile Leu Gln Val Val Lys Tyr Cys Thr Asp Leu Ile Glu Glu
 1185 1190 1195 1200

Lys Asp Leu Glu Lys Leu Asp Leu Val Ile Lys Tyr Met Lys Arg Leu
1205 1210 1215

Met Gln Gln Ser Val Glu Ser Val Trp Asn Met Ala Phe Asp Phe Ile
1220 1225 1230

Leu Asp Asn Val Gln Val Val Leu Gln Gln Thr Tyr Gly Ser Thr Leu
1235 1240 1245

Lys Val Thr
1250

<210> 17

<211> 2957

<212> DNA

<213> Homo sapiens

<220>

<223> apyrimidinic endonuclease 1 (APE1), AP
endonuclease 1, HAP1

<400> 17

ctgcagatag cactggaaa gacaccgcgg aactccgcg agcgagaccc gccaaggccc 60
ctccagggac ctgtcttcct aacgtccagg gagcccgagc caactcgcgc cttacattcg 120
tatccgtttt cctatctctt tcccgtgtc agcccagcct tctccactgt tttttccctc 180
ttgcacagag ttagaatctt aagtcatgtt cacacaatgt gctgtgcac tggcacaacg 240
ataaaacagcc gagggagggt tggggactaa gtgcctagag aatttagagga gggaggcgag 300
gctaagcgtc cgtcacgtgg tgcagacag accaatcacg cgcattttc ggccacgaca 360
agcgcgcctc tgatcacgtg accaggtccg ctacccacgt gggggctcag cgtgcaccc 420
tctttgtgtc cgggttagga ggagcttaggc tgccatcggg ccgggtgcaga tacggggttg 480
ctctttgtc cataagaggg gcttcgtcgg cagtctgaac ggcaagctt agtcaggacc 540
cttaattaag atcctaatt ggctggaggg cagatctcgc gagtagggta caaggcacta 600
tgaatgatc tagttcgtg ggtgagggc tgaagggcct atgatgcacg gaggcgggga 660
aaggatttag agataaacgtg gtttaaaggc gggacctggt gcggggacgc tccttgggag 720
gagtcttctc ccagccttag ctggtttcat gatttcttgc cgtctgttgg caacgcggta 780
aaaatattgc ttcggtgggt gacgcgttac agctgccaa gggcgttgc aacgggaatg 840
ccgaagcgtg ggaaaaaggg agcggtgccg gaagacgggg atgagctcag gacaggtaag 900
ggaatgaaat cagcccttct tcctagaagc tgccgggggg gtgtttgtca ttcccttgc 960
gtacgtaag tacgggcccga ctcatttttgc caggggtttg tgaagaagtc gcaggaaccc 1020
taggcttctg ttgggtctat agttaacgccc ggatcgcagt tggaaaccac cagcttttg 1080
tcagtatata ttactcattt tataagacca gagccaaga agagtaagac ggccgcaaaag 1140
aaaaatgaca aagaggcagc aggagagggc ccagccctgt atgaggaccc cccagatcag 1200
aaaacctcac ccagtgccaa acctgccaca ctcaagatct gctcttggaa tgtggatggg 1260
cttcgaccc ggattaagaa gaaaggatta gatgtgagtg gaatttgagg gaaagagaca 1320
tttttagta ttgaatggtc tttagggtta gtcacccctt ttctccgtt agccttcagg 1380
ctgttttattt tttctcctgc ccgtagttt ctgtggggct tccccagtc tgccagttgt 1440
atttcctaaa tgtctgttcc ttcaacttcca ttgccatttt cttttttagt gttctctcct 1500
cttcccagaa tggcaaaaa acctttcac tataacttccct ccattttatc ttctgcatt 1560
gcattccata tgaagcatgt cctccatccc attaaccata gcttaaaatc ttagcttgc 1620
atccactgccc tatagaaaa acacatctcc ttggcatagc atgtaagact ttcttaccc 1680
tctatattt tttcatttca tctagcttag aattgtttga atattgtgc gcttgactcg 1740
aactccttag gccaagagac tggtaaccc gtgcgtatct atgacttagc atatagatta 1800
ttcaataaat gttctgctga attgataata cgttttccac ctttctttc acttacagtg 1860
ggtaaaggaa gaagccccag atatactgtg cttcaagag accaaatgtt cagagaacaa 1920
actaccagct gaacttcagg agctgcctgg actctctcat caataactgtt cagctccctc 1980
ggacaaggaa gggtacagtg gcgtggccct gcttcccgc cagtgcac tcaaagttc 2040
ttacggcata ggtgagaccc tattgatgcc taatgcctga actcttcaaa accaattgt 2100
aattctctat ctctgccccca cctcttgcatt gcttccctt ttcttatagt ttttatgt 2160
aattctgttt cattttctata ggcgatgagg agcatgatca ggaaggccgg gtgattgtgg 2220
ctgaatttga ctcgtttgtg ctggtaacag catatgtacc taatgcaggc cgaggtctgg 2280

tacgactgga gtaccggcag cgctggatg aagccttcg caagttcctg aagggcctgg 2340
 cttcccgaaa gcccctgtg ctgtgtggag acctcaatgt ggcacatgaa gaaattgacc 2400
 ttgcacaacc caaggggaaac aaaaagaatg ctggcttcac gccacaagag cgccaaggct 2460
 tcgggaaatt actgcaggct gtgccactgg ctgacagctt taggcacctc taccccaaca 2520
 caccctatgc ctacacctt tggacttata tgatgaatgc tcgatccaag aatgttggtt 2580
 ggcccttga ttacttttgc ttgtccact ctctgttacc tgcatgtgt gacagcaaga 2640
 tccgttccaa ggccctcggc agtgatcaact gtctatcac cctataccta gcactgtgac 2700
 accaccccta aatcaacttg agcctggaa ataagcccc tcaactacca ttccttctt 2760
 aaacactt cagagaaatc tgcatctat ttctcatgta taaaactagg aatcctccaa 2820
 ccaggctcct gtgatagagt tcttttaagc ccaagattt ttatggagg gttttttgtt 2880
 ttttaaaaaa aaattgaaca aagactacta atgactttgt ttgaatttac cacatgaaaa 2940
 taaagagcca tagttc 2957

<210> 18
 <211> 318
 <212> PRT
 <213> Homo sapiens

<220>
 <223> apyrimidinic endonuclease 1 (APE1), AP
 endonuclease 1, HAP1

<400> 18
 Met Pro Lys Arg Gly Lys Gly Ala Val Ala Glu Asp Gly Asp Glu
 1 5 10 15

Leu Arg Thr Glu Pro Glu Ala Lys Lys Ser Lys Thr Ala Ala Lys Lys
 20 25 30

Asn Asp Lys Glu Ala Ala Gly Glu Gly Pro Ala Leu Tyr Glu Asp Pro
 35 40 45

Pro Asp Gln Lys Thr Ser Pro Ser Gly Lys Pro Ala Thr Leu Lys Ile
 50 55 60

Cys Ser Trp Asn Val Asp Gly Leu Arg Ala Trp Ile Lys Lys Lys Gly
 65 70 75 80

Leu Asp Trp Val Lys Glu Glu Ala Pro Asp Ile Leu Cys Leu Gln Glu
 85 90 95

Thr Lys Cys Ser Glu Asn Lys Leu Pro Ala Glu Leu Gln Glu Leu Pro
 100 105 110

Gly Leu Ser His Gln Tyr Trp Ser Ala Pro Ser Asp Lys Glu Gly Tyr
 115 120 125

Ser Gly Val Gly Leu Leu Ser Arg Gln Cys Pro Leu Lys Val Ser Tyr
 130 135 140

Gly Ile Gly Asp Glu Glu His Asp Gln Glu Gly Arg Val Ile Val Ala
 145 150 155 160

Glu Phe Asp Ser Phe Val Leu Val Thr Ala Tyr Val Pro Asn Ala Gly
 165 170 175

Arg Gly Leu Val Arg Leu Glu Tyr Arg Gln Arg Trp Asp Glu Ala Phe
 180 185 190

Arg Lys Phe Leu Lys Gly Leu Ala Ser Arg Lys Pro Leu Val Leu Cys
195 200 205

Gly Asp Leu Asn Val Ala His Glu Glu Ile Asp Leu Arg Asn Pro Lys
210 215 220

Gly Asn Lys Lys Asn Ala Gly Phe Thr Pro Gln Glu Ala Gln Gly Phe
225 230 235 240

Gly Glu Leu Leu Gln Ala Val Pro Leu Ala Asp Ser Phe Arg His Leu
245 250 255

Tyr Pro Asn Thr Pro Tyr Ala Tyr Thr Phe Trp Thr Tyr Met Met Asn
260 265 270

Ala Arg Ser Lys Asn Val Gly Trp Arg Leu Asp Tyr Phe Leu Leu Ser
275 280 285

His Ser Leu Leu Pro Ala Leu Cys Asp Ser Lys Ile Arg Ser Lys Ala
290 295 300

Leu Gly Ser Asp His Cys Pro Ile Thr Leu Tyr Leu Ala Leu
305 310 315

<210> 19

<211> 1161

<212> DNA

<213> Homo sapiens

<220>

<223> cyclin-dependent kinase 3 (CDK3), cyclin-dependent protein kinase

<400> 19

ccacatggaa gctggaggag caaccgggag cgctgggctg gggtgcaa at tgcccagtgc 60
cttctgttcc ccaggcagct ctgtggccat ggatatgttc cagaaggtag agaagatcg 120
agagggcacc tatggggtgg tgtacaaggc caagaacagg gagacagggc agctggtggc 180
cctgaagaag atcagactgg atttggagat ggagggggtc ccaagcactg ccatcaggga 240
gatctcgctg ctcaaggaac tgaagcaccc caacatcgtc cgactgctgg acgtggtgc 300
caacgagagg aagctctatc tggtgttga gttcctcagc caggaacctga agaagtacat 360
ggactccacc ccagggctcag agctcccccgc gcacccatc aagagctacc tcttccagct 420
gctgcagggg gtgagttct gccactcaca tcgggtcatc caccgagacc tgaagcccca 480
gaacctgctc atcaatgagt tgggtgcct caagctggct gacttcggcc tggctcgcc 540
cttcgggggtg cccctgcgc ca cctacacca tgaggtggtg acactgtggt atcgcgc 600
cgagattctc ttggcagca agttctatac cacagctgtg gatatctgga gcattgggt 660
catctttgca gagatggtga ctgcggaaagc cctgtttccct ggtgactctg agattgacca 720
gctcttttgt atcttcgta tgctgggac acccagcgaa gacacatggc cccgggtcac 780
ccagctgct gactataagg gcagcttccc taagtggacc aggaaggac tggaaagagat 840
tgtgcccata ctggagccag agggcagggc cctgctcatg caactcctgc agtatgaccc 900
cagccagccg atcacagcca agactgcctt ggcccaccccg tacttctcat cccctgagcc 960
ctccccagct gcccggcact atgtgctgca gcgattccgc cattgagaat gtcaaggcca 1020
cactcagatc ctttctcgag cagcagctgc tgccccagct gcctcctacc cattgccaag 1080
agaggatgca tctggggaga gcaaaggact aaggaattca gcatcagcct gcagagggct 1140
gagtctgggt tagtccctgccc c 1161

<210> 20

<211> 305

<212> PRT

<213> Homo sapiens

<220>
 <223> cyclin-dependent kinase 3 (CDK3), cyclin-dependent
 protein kinase

<400> 20
 Met Asp Met Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
 1 5 10 15

Val Val Tyr Lys Ala Lys Asn Arg Glu Thr Gly Gln Leu Val Ala Leu
 20 25 30

Lys Lys Ile Arg Leu Asp Leu Glu Met Glu Gly Val Pro Ser Thr Ala
 35 40 45

Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Lys His Pro Asn Ile Val
 50 55 60

Arg Leu Leu Asp Val Val His Asn Glu Arg Lys Leu Tyr Leu Val Phe
 65 70 75 80

Glu Phe Leu Ser Gln Asp Leu Lys Tyr Met Asp Ser Thr Pro Gly
 85 90 95

Ser Glu Leu Pro Leu His Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
 100 105 110

Gln Gly Val Ser Phe Cys His Ser His Arg Val Ile His Arg Asp Leu
 115 120 125

Lys Pro Gln Asn Leu Leu Ile Asn Glu Leu Gly Ala Ile Lys Leu Ala
 130 135 140

Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Leu Arg Thr Tyr Thr
 145 150 155 160

His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly
 165 170 175

Ser Lys Phe Tyr Thr Thr Ala Val Asp Ile Trp Ser Ile Gly Cys Ile
 180 185 190

Phe Ala Glu Met Val Thr Arg Lys Ala Leu Phe Pro Gly Asp Ser Glu
 195 200 205

Ile Asp Gln Leu Phe Arg Ile Phe Arg Met Leu Gly Thr Pro Ser Glu
 210 215 220

Asp Thr Trp Pro Gly Val Thr Gln Leu Pro Asp Tyr Lys Gly Ser Phe
 225 230 235 240

Pro Lys Trp Thr Arg Lys Gly Leu Glu Glu Ile Val Pro Asn Leu Glu
 245 250 255

Pro Glu Gly Arg Asp Leu Leu Met Gln Leu Leu Gln Tyr Asp Pro Ser
 260 265 270

Gln Arg Ile Thr Ala Lys Thr Ala Leu Ala His Pro Tyr Phe Ser Ser
 275 280 285

Pro Glu Pro Ser Pro Ala Ala Arg Gln Tyr Val Leu Gln Arg Phe Arg
290 295 300

His
305

```
<210> 21
<211> 2297
<212> DNA
<213> Homo sapiens

<220>
<223> PIM1 oncogene serine threonine kinase
```

```
<220>
<221> modified_base
<222> (1896)..(1906)
<223> n = g, a, c or t
```

<400> 21
gccccgcac tcggagggtt ggatgctctt gtccaaaatc aactcgcttg cccacccctgc 60
cgccccgcgc tgcaacgacc tgcacgccac caagctggcg ccgggcaagg agaaggagcc 120
cctggagtcg cagtaccagg tggggcccgct actgggcagc ggccgcttcg gctcggtcta 180
ctcaggccatc cgcgctcccg acaacttgcc ggtggccatc aaacacgtgg agaaggaccg 240
gatttccgac tggggagagc tgccataatgg cactcgagtg cccatggaag tggtcctgct 300
gaagaaggtg agctcggtt tctccggcgat cattaggctc ctggacttgt tcgagaggcc 360
cgacagtttgc tccctgatcc tggagaggcc cgagccgtg caagatctct tcgacttcat 420
cacggaaagg ggagccctgc aagaggagct ggcccgccagc ttcttctggc aggtgctgga 480
ggccgtgcgg cactgccaca actgcggggt gctccaccgc gacatcaagg acgaaaacat 540
ccttatcgac ctcataatcgcc gcgagctcaa gctcatcgac ttccgggtcgg gggcgctgct 600
caaggacacc gtctacacgg acttcgatgg gaccggagtg tataggccctc cagagtggat 660
ccgctaccat cgctaccatcg gcaggcgcc ggcagtcctgg tccctgggga tcctgctgta 720
tgatatgggtg tggggagata ttcccttcga gcatgacgaa gagatcatca gggggccagg 780
tttcttcagg cagagggtct cttcagaatg tcagcatctc attagatggt gcttggccct 840
gagaccatca gataggccaa cttcgaaga aatccagaac catccatggc tgcaagatgt 900
tctctgccc caggaaactg ctgagatcca cttccacacgc ctgtcgccgg gccccagcaa 960
atagcagcct ttctggcagg tcctccctc tcttgcaga tgcccaggag ggaagcttct 1020
gtctccagct ttcccgagta ccagtgcacac gtctcgccaa gcaggacagt gcttgataca 1080
ggaacaacat ttacaactca ttccagatcc caggccctg gaggctgcct cccaacagtg 1140
gggaagagtg actctccagg ggtccctaggc ctcaactccct cccatagata ctctcttctt 1200
ctcataggtg tccagcattt ctggactctg aaatatcccg ggggtggggg gtgggggtgg 1260
gtcagaaccc tgccatggaa ctgttccct catcatgagt tctgctgaat gccgcgatgg 1320
gtcaggttagg gggaaacag gttgggatgg gataggacta gcaccattt aagtccctgt 1380
cacctcttcc gactctttctt gagtgccttctc tggggact ccggctgtgc tgggagaaat 1440
acttgaactt gcctctttta cctgtgtctt ctccaaaaat ctgcctgggt tttgttccct 1500
atttttctct cctgtctccct ctcacccccc cttcatatg aaagggtgcca tggaaagaggc 1560
tacaggccaa aacgctgagc cacctgcctt ttttctctt cctttagtaa aactccgagt 1620
gaactggctc tcctttttgg ttttactta actgtttcaa agccaagacc tcacacacac 1680
aaaaaaatgca caaacaatgc aatcaacaga aaagctgtaa atgtgtgtac agttggcatg 1740
gtagtatatac aaaagattgt agtggatcta attttaaga aattttgcct ttaagttatt 1800
ttacctgttt ttgtttctt ttttggaaaga tgcgcatctt aactctggagg tcaatgttat 1860
gtatattatc atttattat ttgggtccct tcctannnnn nnnnnnngctg ctgccttagt 1920
tttcttcctt ccttcctcc tctgtactgg ggaccttttgg ggggaggggct ggcacgcttg 1980
ctctgtttgt ggggtgacgg gactcaggcg ggacagtgtct gcaactccct ggcttctgt 2040
ggggccctca cctacttacc caggtgggtc ccggctctgt ggggtgatggg gagggggcatt 2100
gctgactgtg tatataaggat aattatgaaa agcagttctg gatgggtgtgc cttccagatc 2160
ctctctgggg ctgtgttttgg agcagcaggat agcctgtctt gtttatctga gtgaaataact 2220
gtacagggga ataaaaagaga tcttattttt tttttatac ttggcggttt ttgaataaaaa 2280
acctttgtc taaaaac 2297

<210> 22
 <211> 313
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PIM1 oncogene serine threonine kinase

<400> 22
 Met Leu Leu Ser Lys Ile Asn Ser Leu Ala His Leu Arg Ala Arg Ala
 1 5 10 15

Cys Asn Asp Leu His Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu
 20 25 30

Pro Leu Glu Ser Gln Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly
 35 40 45

Phe Gly Ser Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val
 50 55 60

Ala Ile Lys His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu
 65 70 75 80

Pro Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val
 85 90 95

Ser Ser Gly Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg
 100 105 110

Pro Asp Ser Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp
 115 120 125

Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala
 130 135 140

Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn
 145 150 155 160

Cys Gly Val Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp
 165 170 175

Leu Asn Arg Gly Glu Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu
 180 185 190

Leu Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser
 195 200 205

Pro Pro Glu Trp Ile Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala
 210 215 220

Val Trp Ser Leu Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile
 225 230 235 240

Pro Phe Glu His Asp Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg
 245 250 255

Gln Arg Val Ser Ser Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala
 260 265 270

Leu Arg Pro Ser Asp Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro
275 280 285

Trp Met Gln Asp Val Leu Leu Pro Gln Glu Thr Ala Glu Ile His Leu
290 295 300

His Ser Leu Ser Pro Gly Pro Ser Lys
305 310

```
<210> 23
<211> 3178
<212> DNA
<213> Homo sapiens
```

<220>
<223> CDC7 cell division cycle 7 (CDC7), CDC7 cell
division cycle 7-like 1 (CDC7L1) protein serine
threonine kinase

<400> 23
gatctttgg agacggcgac ccaggcatct ggggagccac agaagtcgta ctccttaaa 60
ccctgtttg cttccccctgt ggatgttaacc ccttagctgg cattttgcat ctcaattggc 120
ttgtgatgga ggcgttttgg gggattcaga tggatgagcc aatggcttt tctccccagc 180
gtgaccgggtt tcaggctgaa ggcttttaaa aaaaaaaacga gcagaatttt aaacttgcag 240
gtgttaaaaa agatatttag aagctttatg aagctgtacc acagcttagt aatgtgttta 300
agattgagga caaaattgga gaaggcactt tcagctctgt ttatggcc acagcacagt 360
tacaagtagg acctgaagag aaaattgctc taaaacactt gattcaaca agtcatccta 420
taagaattgc agctgaactt cagtgccctaa cagtggttgg gggcaagat aatgtcatgg 480
gagttaaata ctgctttagg aagaatgatc atgttagttat tgctatgcca tatctggagc 540
atgagtcgtt tttggacatt ctgaattctc tttccttca agaagtacgg gaatatatgc 600
ttaatctgtt caaagcttt aaacgcattt atcagtttg tattgttac cgtgatgtta 660
agcccagcaa tttttatataat aataggcgcc tgaaaaagta tgccttggta gactttgggt 720
tggcccaagg aacccatgt acgaaaaatag agcttcttaa atttgtccag tctgaagctc 780
agcagggaaag gtgttcacaa aacaaatccc acataatcac agggaaacaag attccactga 840
gtggcccaagt acctaaggag ctggatcagc agtccacac aaaagcttct gttaaaagac 900
cctacacaaa tgaccaaattt cagattaaac aaggaaaaaga cgaaaaaggag ggtatctgttag 960
gcctttctgt ccagcgctct gttttggag aaagaaaattt caatatacac agtccattt 1020
cacatgagag ccctgcagtg aaactcatga agcagtcaaa gactgtggat gtactgtcta 1080
gaaagttagc aacaaaaaaag aaggctattt ctacgaaagt tatgaatagt gctgtgatga 1140
ggaaaactgc cagttcttgc ccagctagcc tgacctgtga ctgctatgca acagataaaag 1200
ttttagtat ttgccttca aggctgcagc aggttgcqcc tagggcaggt acaccaggat 1260
tcagagcacc agaggtctt acaaagtgcc ccaatcaaac tacagcaattt gacatgtgtt 1320
ctgcagggtt catatttctt tctttgctt gtggacgata tccattttt aaagcaagtg 1380
atgatttaac tgctttggcc caaattatga caatttagggg atccagagaa actatccaag 1440
ctgctaaaac ttttggaaa tcaatattat gtagcaaga agtccagca caagacttga 1500
gaaaactctg tgagagactc aggggtatgg attctagcac tcccaagttt acaagtgata 1560
tacaaggcga tgcttctcat caaccagcta tttcagagaa gactgaccat aaagcttctt 1620
gcctcggtca aacacctcca ggacaataact cagggaaattt catttttttggatgatgt 1680
atagctgtga gcattgtttt gatgagtata ataccaattt agaaggctgg aatgaggtac 1740
ctgatgaagc ttatgacctg cttgataaaac ttcttagatct aaatccagct tcaagaataa 1800
cagcagaaga agctttgtt catccatttt ttaaagatataat gagttgtga taatggatct 1860
tcatttaatg ttactgtta tgaggttagaa taaaaaaagaa tactttgtaa tagccacaag 1920
ttcttggtttta gagaccagag caggattaat aattttttt aacatttttag tggttgg 1980
cacattctaa aatatacgatt aagaataactt aaaatgcctg ggatagttct tgggactaac 2040
aacatgatct tctttgagtt aaacccatctt aagtagattt taggtgggtt cctattaggt 2100
cagattttta gctccctaa ttacccctca ctgacataca gaaaaaggag cagtttttagt 2160
ttaattaaat taaaattaaac agatgtgtatc aggattaaat gaatcaaaaag acttaattt 2220
tagattctt tagagttatc agcttaggtat agtttgggaa aactcaaccc ggtgctgggt 2280
ctcttaacaa ttttgttaat aaagaagata atttcctttt ctagaggtac atattaggcc 2340
tttatgaaac actaaaacaa tgaggaaatg ttgtcatqq ggcaaaagttt cacttaaaat 2400

tgaattcattttaaa aaacacttca taaaaggcatt ctgggtgtcaa ttgccat 2460
 tttcttactg gcttctcaat ttcttcctt ctctgcccctt acctaaaaca ttctcctcg 2520
 aaattacatg gtgctgacca caaagtttctt ggatgttttta ttaaatatttacgtgtt 2580
 cagttggaa tttaaaaataa tacatacact ggttgataaa gggaaagctgc aggaccaagg 2640
 tgaagattga tagtccaaat gctttctt tttgagttgt atattttc acaccatctt 2700
 agatataatt aggttagctgc tgaaaggaaa agtgaataca gaattgacgg tattattg 2760
 gattttcctt ctgcgttagag ccatccagat ctctgtatcc tggtttgact aagtctttagg 2820
 tgggtggaa agacagataa tgaagtaggc aaagagaaaa ggacccaaga tagaggtt 2880
 tattcagaaa tggtatataat caatgacagc atatcaaact tcctatggaa aaaagtctgg 2940
 tgggtggtca gctgacagat ttccatataa gtagtcatag aatacagaaa tagtttagg 3000
 acatgtattc atttgttat tttgagcatt gataggtcag tatatctacc taatctgtt 3060
 ggtaagtataa ggatataaa accattacca ttgatctgtc ttatgccata atcttaaaa 3120
 aaaattgaat ttgtatattc aataaagtta tcctttata aaaaaaaaaa 3178

<210> 24
 <211> 574
 <212> PRT
 <213> Homo sapiens

<220>
 <223> CDC7 cell division cycle 7 (CDC7), CDC7 cell
 division cycle 7-like 1 (CDC7L1) protein serine
 threonine kinase

<400> 24
 Met Glu Ala Ser Leu Gly Ile Gln Met Asp Glu Pro Met Ala Phe Ser
 1 5 10 15

 Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys Lys Asn Glu
 20 25 30

 Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu Lys Leu Tyr
 35 40 45

 Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu Asp Lys Ile
 50 55 60

 Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala Gln Leu Gln
 65 70 75 80

 Val Gly Pro Glu Glu Lys Ile Ala Leu Lys His Leu Ile Pro Thr Ser
 85 90 95

 His Pro Ile Arg Ile Ala Ala Glu Leu Gln Cys Leu Thr Val Ala Gly
 100 105 110

 Gly Gln Asp Asn Val Met Gly Val Lys Tyr Cys Phe Arg Lys Asn Asp
 115 120 125

 His Val Val Ile Ala Met Pro Tyr Leu Glu His Glu Ser Phe Leu Asp
 130 135 140

 Ile Leu Asn Ser Leu Ser Phe Gln Glu Val Arg Glu Tyr Met Leu Asn
 145 150 155 160

 Leu Phe Lys Ala Leu Lys Arg Ile His Gln Phe Gly Ile Val His Arg
 165 170 175

 Asp Val Lys Pro Ser Asn Phe Leu Tyr Asn Arg Arg Leu Lys Lys Tyr
 180 185 190

Ala Leu Val Asp Phe Gly Leu Ala Gln Gly Thr His Asp Thr Lys Ile
 195 200 205
 Glu Leu Leu Lys Phe Val Gln Ser Glu Ala Gln Gln Glu Arg Cys Ser
 210 215 220
 Gln Asn Lys Ser His Ile Ile Thr Gly Asn Lys Ile Pro Leu Ser Gly
 225 230 235 240
 Pro Val Pro Lys Glu Leu Asp Gln Gln Ser Thr Thr Lys Ala Ser Val
 245 250 255
 Lys Arg Pro Tyr Thr Asn Ala Gln Ile Gln Ile Lys Gln Gly Lys Asp
 260 265 270
 Gly Lys Glu Gly Ser Val Gly Leu Ser Val Gln Arg Ser Val Phe Gly
 275 280 285
 Glu Arg Asn Phe Asn Ile His Ser Ser Ile Ser His Glu Ser Pro Ala
 290 295 300
 Val Lys Leu Met Lys Gln Ser Lys Thr Val Asp Val Leu Ser Arg Lys
 305 310 315 320
 Leu Ala Thr Lys Lys Lys Ala Ile Ser Thr Lys Val Met Asn Ser Ala
 325 330 335
 Val Met Arg Lys Thr Ala Ser Ser Cys Pro Ala Ser Leu Thr Cys Asp
 340 345 350
 Cys Tyr Ala Thr Asp Lys Val Cys Ser Ile Cys Leu Ser Arg Arg Gln
 355 360 365
 Gln Val Ala Pro Arg Ala Gly Thr Pro Gly Phe Arg Ala Pro Glu Val
 370 375 380
 Leu Thr Lys Cys Pro Asn Gln Thr Thr Ala Ile Asp Met Trp Ser Ala
 385 390 395 400
 Gly Val Ile Phe Leu Ser Leu Leu Ser Gly Arg Tyr Pro Phe Tyr Lys
 405 410 415
 Ala Ser Asp Asp Leu Thr Ala Leu Ala Gln Ile Met Thr Ile Arg Gly
 420 425 430
 Ser Arg Glu Thr Ile Gln Ala Ala Lys Thr Phe Gly Lys Ser Ile Leu
 435 440 445
 Cys Ser Lys Glu Val Pro Ala Gln Asp Leu Arg Lys Leu Cys Glu Arg
 450 455 460
 Leu Arg Gly Met Asp Ser Ser Thr Pro Lys Leu Thr Ser Asp Ile Gln
 465 470 475 480
 Gly His Ala Ser His Gln Pro Ala Ile Ser Glu Lys Thr Asp His Lys
 485 490 495
 Ala Ser Cys Leu Val Gln Thr Pro Pro Gly Gln Tyr Ser Gly Asn Ser
 500 505 510

Phe Lys Lys Gly Asp Ser Asn Ser Cys Glu His Cys Phe Asp Glu Tyr
515 520 525

Asn Thr Asn Leu Glu Gly Trp Asn Glu Val Pro Asp Glu Ala Tyr Asp
530 535 540

Leu Leu Asp Lys Leu Leu Asp Leu Asn Pro Ala Ser Arg Ile Thr Ala
545 550 555 560

Glu Glu Ala Leu Leu His Pro Phe Phe Lys Asp Met Ser Leu
565 570

<210> 25

<211> 1427

<212> DNA

<213> Homo sapiens

<220>

<223> cyclin-dependent kinase 7 (CDK7), kinase subunit
of Cdk-activating kinase (CAK), kinase component
of transcription factor complex TFIIH

<400> 25

tgggtgttgg aggctttaag gtagcttaaattcgtttg tcctggagc tcgcctttt 60
cggctggagt cggctttac ggccggat ggctctggac gtgaagtctc gggcaaagcg 120
ttatgagaag ctggacttcc ttggggaggg acagttgcc accgttaca aggccagaga 180
taagaataacc aaccaaatttgcgccattaa gaaaatcaaa cttggacata gatcagaagc 240
taaagatggt ataaatagaa ccgccttaag agagataaaa ttattacagg agctaagtca 300
tccaaatata attggcttcc ttgatgttttggacataaaa tctaattatgccttgc 360
tgatTTATG gaaaactgatc tagaggttat aataaaggat aatagtttg tgctgacacc 420
atcacacatc aaaggctaca tggtgtatc tcttcaagga tttagatatt tacatcaaca 480
ttggatccta catagggatc tgaaacccaaa caacttgcgttgcgtatgaaa atggagttct 540
aaaactggca gattttggcc tggccaaatc tttggggagc cccaaatagag cttatacaca 600
tcaggttgc accaggttgt atcggggcccc cgagttacta tttggagcttggatgtatgg 660
tgtaggtgtg gacatgtggg ctgttggttgc tatattagca gagttacttc taagggttcc 720
tttttgcga ggagattcag accttgcata gctaaacaaga atattgaaa ctttgggcac 780
accaactggag gaacagtggc cggacatgttgc tagtcttca gattatgtga catttaagag 840
tttcccttgcg atacatcttgc atcacatctt cagtgacatc ggagacgact tactagatct 900
catacaaggc ttatttttat ttaatccatg tgctcgaattt acggccacac aggcaactgaa 960
aatgaagtat ttcaatcggcc aacacatggc ttgcgtatgc caagacccaaa 1020
ctgtccagtg gaaaccttaaaggagcaatc aaatccagct ttggcaataa aaaggaaaaag 1080
aacagaggcc tttagaacaag gaggatttgc caagaaaacta atttttaaa gagaacactg 1140
gacaacatt tactactgag ggaaatagcc aaaaaggcaa ataatggaaa aatagtaaac 1200
attaagtaaa tgctgttagaa gtgagttgttgc ttgtatcttgc cacatgtaaa atatgtaaaa 1260
ctatgggtta tttttattaa atgtatttta aaataaaaaat ttaattctgg tttttctgat 1320
tagagtccca aagtgagaaa agttcaatac tcttggaaatg tagaattgaa aatgcattag 1380
ggaaaaactta ataaaaatttttgcgtatgc ttggaaaaaaa aaaaaaaa 1427

<210> 26

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<223> cyclin-dependent kinase 7 (CDK7), kinase subunit
of Cdk-activating kinase (CAK), kinase component
of transcription factor complex TFIIH

<400> 26
 Met Ala Leu Asp Val Lys Ser Arg Ala Lys Arg Tyr Glu Lys Leu Asp
 1 5 10 15
 Phe Leu Gly Glu Gly Gln Phe Ala Thr Val Tyr Lys Ala Arg Asp Lys
 20 25 30
 Asn Thr Asn Gln Ile Val Ala Ile Lys Lys Ile Lys Leu Gly His Arg
 35 40 45
 Ser Glu Ala Lys Asp Gly Ile Asn Arg Thr Ala Leu Arg Glu Ile Lys
 50 55 60
 Leu Leu Gln Glu Leu Ser His Pro Asn Ile Ile Gly Leu Leu Asp Ala
 65 70 75 80
 Phe Gly His Lys Ser Asn Ile Ser Leu Val Phe Asp Phe Met Glu Thr
 85 90 95
 Asp Leu Glu Val Ile Ile Lys Asp Asn Ser Leu Val Leu Thr Pro Ser
 100 105 110
 His Ile Lys Ala Tyr Met Leu Met Thr Leu Gln Gly Leu Glu Tyr Leu
 115 120 125
 His Gln His Trp Ile Leu His Arg Asp Leu Lys Pro Asn Asn Leu Leu
 130 135 140
 Leu Asp Glu Asn Gly Val Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys
 145 150 155 160
 Ser Phe Gly Ser Pro Asn Arg Ala Tyr Thr His Gln Val Val Thr Arg
 165 170 175
 Trp Tyr Arg Ala Pro Glu Leu Leu Phe Gly Ala Arg Met Tyr Gly Val
 180 185 190
 Gly Val Asp Met Trp Ala Val Gly Cys Ile Leu Ala Glu Leu Leu Leu
 195 200 205
 Arg Val Pro Phe Leu Pro Gly Asp Ser Asp Leu Asp Gln Leu Thr Arg
 210 215 220
 Ile Phe Glu Thr Leu Gly Thr Pro Thr Glu Glu Gln Trp Pro Asp Met
 225 230 235 240
 Cys Ser Leu Pro Asp Tyr Val Thr Phe Lys Ser Phe Pro Gly Ile Pro
 245 250 255
 Leu His His Ile Phe Ser Ala Ala Gly Asp Asp Leu Leu Asp Leu Ile
 260 265 270
 Gln Gly Leu Phe Leu Phe Asn Pro Cys Ala Arg Ile Thr Ala Thr Gln
 275 280 285
 Ala Leu Lys Met Lys Tyr Phe Ser Asn Arg Pro Gly Pro Thr Pro Gly
 290 295 300
 Cys Gln Leu Pro Arg Pro Asn Cys Pro Val Glu Thr Leu Lys Glu Gln
 305 310 315 320

Ser Asn Pro Ala Leu Ala Ile Lys Arg Lys Arg Thr Glu Ala Leu Glu
325 330 335

Gln Gly Gly Leu Pro Lys Lys Leu Ile Phe
340 345

<210> 27
<211> 2169
<212> DNA
<213> Homo sapiens

<220>
<223> cytokine-inducible kinase (CNK) serine threonine kinase, proliferation-related kinase (PRK), polo-like kinase 3 (PLK3)

<400> 27
ccgcctccga gtgccttgcg cggacctgag ctggagatgc tggccggct accgacgtca 60
gaccggggc gcctcatcac ggacccggc agcggccgca cctacccaa aggccgcttg 120
ttggcaagg ggggcttcgc ccgctgtac gaggccactg acacagagac tggcagcgcc 180
tacgctgtca aagtcatccc gcagagccgc gtgcacaagg cgcatcagcg cgagaagatc 240
ctaaatgaga ttgagctgca ccgagacctg cagcaccggc acatctgtcg ttttcgac 300
cacttgagg acgctgacaa catctacatt ttcttgagg tctgcagccg aaagtccctg 360
gcccacatct ggaaggcccg gcacaccctg ttggagccag aagtgcgcta ctacctgccc 420
cagatccctt ctggcctcaa gtacttgac cagcggcga tcttgcacccg ggacctaag 480
ttggaaatt ttttcatcac tgagaacatg gaactgaagg tgggggattt tgggctggca 540
gcccgggttgg agcctccgga gcagaggaag aagaccatct gtggcaccccc caactatgtg 600
gctccagaag tgctgctgag acagggccac ggcctgaaag cgatgtatg gtcactggc 660
tgtgtcatgt acacgctgct ctgcgggagc cctcccttg agacggctga cctgaaggag 720
acgtaccgct gcatcaagca gtttcaactac acgctgcctg ccagcccttc actgcctgcc 780
cggcagctcc tggccgccc cttcgggccc tcacccccc accgccccctc tattgaccag 840
atcctgccc atgacttctt taccaggc tacacccccc atcgactccc tatcagcagc 900
tgcgtgacag tcccgacact gacacccccc aaccacgcta ggagtctgtt tgccaaagtt 960
accaagagcc tctttggcag aaagaagaag agtaagaatc atgcccagga gagggatgag 1020
gtctccgggt tggtagcgg ctttgcgc acatccgtt gccatcagga tgccaggcca 1080
gaggctccag cagcttctgg cccagccct gtcaagctgg tagagacagc acctgaagac 1140
agctcacccc gtggacact ggcaagcagt ggagatggat ttgaagaagg tctgactgtg 1200
gccacagttag tggagtccgc ctttgcgtt ctgagaaatt gtatagctt catgccccca 1260
gcggAACAGA accccggcccc cctggcccg ccagacccctc tggtagggat cagcaagtgg 1320
gttactact ccaataagtt cggctttggg tatcaactgt ccagccccc tggactgtg 1380
ctcttcaacg atggcacaca tatggccctg tcggccaaaca gaaagactgt gcaactacaat 1440
cccaccagca caaagcactt ctccttcctt gtgggtgctg tgccccggc cctgcagcct 1500
cagctggta tcctgcccgtt cttcccttcc tacatggagc agcacccat gaagggtgaa 1560
gatctgccc gtgtggaaaga ggtagagta cttgcgtccgc cttgcgtgt gcaactggc 1620
aagacggatc aggctctcct catgctgttt agttagatggca ctgtccaggt gaaacttctac 1680
ggggaccaca ccaagctgat tctcactggc tggagccccc tccttgcgtt ttttgcgtt 1740
cgaaatcgta gtgcttgcgtt ttaccccttcc tccaccccttcc ggcagctggg ctgctctcca 1800
gacccgtggc agcgtactccg ctatgctctg cgcctgctcc gggaccggcag cccagcttag 1860
gacccaaagcc ctgaaggcctt gaggccctgt cttgcgtccgc tctggccctt gcctttgtgg 1920
ccttcccccctt tccttgcgtt cttcactggc ggctttggc cgaatcccccc agggaaatcag 1980
ggaccagctt tactggagtt gggggcgct tggtagccgtt ggctccctacc ccatctccaa 2040
gataaggctg agccttagct cccagctagg gggcggttatt tatggaccac ttttatttat 2100
tgtcagacac ttattttattt ggtatgtgagc cccagggggc ctcctccctt gataataaac 2160
aatttttgc 2169

<210> 28
<211> 607
<212> PRT
<213> Homo sapiens

<220>

<223> cytokine-inducible kinase (CNK) serine threonine kinase, proliferation-related kinase (PRK), polo-like kinase 3 (PLK3)

<400> 28

Met Leu Ala Gly Leu Pro Thr Ser Asp Pro Gly Arg Leu Ile Thr Asp
1 5 10 15

Pro Arg Ser Gly Arg Thr Tyr Leu Lys Gly Arg Leu Leu Gly Lys Gly
20 25 30

Gly Phe Ala Arg Cys Tyr Glu Ala Thr Asp Thr Glu Thr Gly Ser Ala
35 40 45

Tyr Ala Val Lys Val Ile Pro Gln Ser Arg Val Ala Lys Pro His Gln
50 55 60

Arg Glu Lys Ile Leu Asn Glu Ile Glu Leu His Arg Asp Leu Gln His
65 70 75 80

Arg His Ile Val Arg Phe Ser His His Phe Glu Asp Ala Asp Asn Ile
85 90 95

Tyr Ile Phe Leu Glu Leu Cys Ser Arg Lys Ser Leu Ala His Ile Trp
100 105 110

Lys Ala Arg His Thr Leu Leu Glu Pro Glu Val Arg Tyr Tyr Leu Arg
115 120 125

Gln Ile Leu Ser Gly Leu Lys Tyr Leu His Gln Arg Gly Ile Leu His
130 135 140

Arg Asp Leu Lys Leu Gly Asn Phe Phe Ile Thr Glu Asn Met Glu Leu
145 150 155 160

Lys Val Gly Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Pro Glu Gln
165 170 175

Arg Lys Lys Thr Ile Cys Gly Thr Pro Asn Tyr Val Ala Pro Glu Val
180 185 190

Leu Leu Arg Gln Gly His Gly Pro Glu Ala Asp Val Trp Ser Leu Gly
195 200 205

Cys Val Met Tyr Thr Leu Leu Cys Gly Ser Pro Pro Phe Glu Thr Ala
210 215 220

Asp Leu Lys Glu Thr Tyr Arg Cys Ile Lys Gln Val His Tyr Thr Leu
225 230 235 240

Pro Ala Ser Leu Ser Leu Pro Ala Arg Gln Leu Leu Ala Ala Ile Leu
245 250 255

Arg Ala Ser Pro Arg Asp Arg Pro Ser Ile Asp Gln Ile Leu Arg His
260 265 270

Asp Phe Phe Thr Lys Gly Tyr Thr Pro Asp Arg Leu Pro Ile Ser Ser
275 280 285

Cys Val Thr Val Pro Asp Leu Thr Pro Pro Asn Pro Ala Arg Ser Leu
 290 295 300
 Phe Ala Lys Val Thr Lys Ser Leu Phe Gly Arg Lys Lys Lys Ser Lys
 305 310 315 320
 Asn His Ala Gln Glu Arg Asp Glu Val Ser Gly Leu Val Ser Gly Leu
 325 330 335
 Met Arg Thr Ser Val Gly His Gln Asp Ala Arg Pro Glu Ala Pro Ala
 340 345 350
 Ala Ser Gly Pro Ala Pro Val Ser Leu Val Glu Thr Ala Pro Glu Asp
 355 360 365
 Ser Ser Pro Arg Gly Thr Leu Ala Ser Ser Gly Asp Gly Phe Glu Glu
 370 375 380
 Gly Leu Thr Val Ala Thr Val Val Glu Ser Ala Leu Cys Ala Leu Arg
 385 390 395 400
 Asn Cys Ile Ala Phe Met Pro Pro Ala Glu Gln Asn Pro Ala Pro Leu
 405 410 415
 Ala Gln Pro Glu Pro Leu Val Trp Val Ser Lys Trp Val Asp Tyr Ser
 420 425 430
 Asn Lys Phe Gly Phe Gly Tyr Gln Leu Ser Ser Arg Arg Val Ala Val
 435 440 445
 Leu Phe Asn Asp Gly Thr His Met Ala Leu Ser Ala Asn Arg Lys Thr
 450 455 460
 Val His Tyr Asn Pro Thr Ser Thr Lys His Phe Ser Phe Ser Val Gly
 465 470 475 480
 Ala Val Pro Arg Ala Leu Gln Pro Gln Leu Gly Ile Leu Arg Tyr Phe
 485 490 495
 Ala Ser Tyr Met Glu Gln His Leu Met Lys Gly Gly Asp Leu Pro Ser
 500 505 510
 Val Glu Glu Val Glu Val Pro Ala Pro Pro Leu Leu Leu Gln Trp Val
 515 520 525
 Lys Thr Asp Gln Ala Leu Leu Met Leu Phe Ser Asp Gly Thr Val Gln
 530 535 540
 Val Asn Phe Tyr Gly Asp His Thr Lys Leu Ile Leu Ser Gly Trp Glu
 545 550 555 560
 Pro Leu Leu Val Thr Phe Val Ala Arg Asn Arg Ser Ala Cys Thr Tyr
 565 570 575
 Leu Ala Ser His Leu Arg Gln Leu Gly Cys Ser Pro Asp Leu Arg Gln
 580 585 590
 Arg Leu Arg Tyr Ala Leu Arg Leu Leu Arg Asp Arg Ser Pro Ala
 595 600 605

<210> 29
<211> 1321
<212> DNA
<213> Homo sapiens

<220>
<223> potentially prenylated protein tyrosine
phosphatase (PRL-3), protein tyrosine phosphatase
type IVA, member 3, isoform 2, transcript variant
2 (PTP4A3)

<400> 29
tgactatcca gctctgagag acgggagttt ggagttgccccc gctttactttt ggttgggttg 60
ggggggccgg cgggctgttt tggccctttt ctttttaag agttgggttt tcttttttaa 120
ttatccaaac agtgggcagc ttccctcccc acacccaagt atttgaccaa tatttgcg 180
gggtatgggg gttgggtttt aaatctcggt tctcttgac aagcacaggg atctcggtt 240
cctcatttt tgggggtgtg tggggacttc tcaggtcggt tcccccagcct tctctgcagt 300
cccttcgtcc ctggccgggccc cgtccgggagg cgccatggct cggatgaacc gcccggcccc 360
ggtggaggtg agctacaaac acatgcgtt cctcatcacc cacaacccca ccaacgcac 420
gctcagcacc ttcatgtgagg acctgaagaa gtacggggtt accactgtgg tgcgtgtgtg 480
tgaagtgacc tatgacaaaaa cggccgtgga gaaggatggc atcaccgttg tggactggcc 540
gtttgacgat ggggcgcccc cggccggcaaa ggttagtgaa gactggctga gcctgggtgaa 600
ggccaaagtcc tggaggccc cggcagctg cgtggctgtg cactgcgtgg cgggcctggg 660
ccggaaagcgc cggcggagcca tcaacagcaa gcagctcacc tacctggaga aataccggcc 720
caaacagagg ctgcgggttca aagacccaca cacgcacaag accccgggtct gcgttatgta 780
gctcagacc ttggctgggc ctggctgtca tggtaggtcag gaccttggtt ggacctggag 840
gccctggccca gccctgcttccc gcccagccca gcaggggtctc caggccttgg ctggccccac 900
atcgccctttt cctcccccggac acctccgtgc acttgtgtcc gaggagcgag gagccctcg 960
ggccctgggtt ggcctctggg ccctttctcc tggccctccactccctctg gcggcgtcg 1020
ccgtggctct gtcctctctga ggtgggtcgg ggcggccctctg cccggccccc cccacaccag 1080
ccaggctgggtt ctccctcttagc ctgtttgttgg tgggggtgggg gtatattttg taaccactgg 1140
gccccccagcc cctcttttgc gacccttgc cttggacccctgt tctcgccacc ttaaaattattt 1200
agaccccccggg gcagtcaggt gctccggaca cccgaaggca ataaaacagg agccgtgaaa 1260
aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1320
a 1321

Val Val Asp Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Gly Lys Val
65 70 75 80

Val Glu Asp Trp Leu Ser Leu Val Lys Ala Lys Phe Cys Glu Ala Pro
85 90 95

Gly Ser Cys Val Ala Val His Cys Val Ala Gly Leu Gly Arg Lys Arg
100 105 110

Arg Gly Ala Ile Asn Ser Lys Gln Leu Thr Tyr Leu Glu Lys Tyr Arg
115 120 125

Pro Lys Gln Arg Leu Arg Phe Lys Asp Pro His Thr His Lys Thr Arg
130 135 140

Cys Cys Val Met
145

<210> 31

<211> 3696

<212> DNA

<213> Homo sapiens

<220>

<223> serine threonine kinase 2 (STK2, NEK4)

<400> 31

ggatcgctat ggcagcggcg tcgtcgccgg ccggggccca gcaatccgc cggggcccg 60
ctgcctcaac agccgcccc actgccccct ctccggcatg aaccgagctt cttgttgcgg 120
cccgctgccc taccggccgc tgccgcccga tcccgactct gggccagcgc tgggaacatg 180
ccccctggccg cctactgcta cctgcgggtc gtgggcaagg ggagctatgg agaggtgacg 240
cttgcgtgaaggc accggcggga cggcaagcag tatgtcatca aaaaactgaa cctccgaaat 300
gcctctagcc gagagcggcg agctgctgaa cagaagccc agctctgtc tcagttgaag 360
catcccaaca ttgtcaccta caaggagtca tgggaaggag gagatggtct gctctacatt 420
gtcatgggct tctgtgaagg aggtgatttg taccgaaagc tcaaggagca gaaagggcag 480
cttctgcctg agaatcaggt ggttagtgg tttgtacaga tcgcccattggc tttgcagtat 540
ttacatgaaa aacacatcct tcacatcgagat ctgaaaactc aaaatgtctt cctaacaaga 600
acaaacatca tcaaagttagg ggacctagga attgcccggag ttttagagaa ccactgtgac 660
atggcttagca ccctcattgg cacaccctac tacatgagcc ctgaattgtt ctcaaacaata 720
ccctacaact ataagtctga tggggctt cttaggtct gtgtctatga aatggccacc 780
ttgaagcatg ctttcaatgc aaaagatatg aattctttttag tttatcgat tattgaagga 840
aagctgccac caatgccaag agattacagc ccagagctgg cagaactgtat aagaacaatg 900
ctgagcaaaa ggcctgaaga aaggccgtct gtgaggagca tcctgaggca gccttatata 960
aagcggcaaa tctccatttt tttggagggcc acaaagataa aaacctccaa aaataacatt 1020
aaaaatggtg actctcaatc caagccttt gctacagtgg tttctggaga ggcagaatca 1080
aatcatgaag taatccaccc ccaaccactc tcttctgagg gctcccagac atatataatg 1140
ggtaaggca aatgtttgtc ccaggagaaa cccagggctt ctggctcttt gaagtcacct 1200
gccagtctga aagcccatac ctgcaaacag gactttagca ataccacaga actagccaca 1260
atcagtagcg taaatattga catcttaccc gcaaaaggga gggattcagt gaggatgtgc 1320
tttgcgttccagg agaatcagcc aagatatttg gatgcctcta atgagttagg aggttatatgc 1380
agtatttctc aagtggaga ggagatgtg caggacaaca ctaaatccag tgcccagct 1440
gaaaacctga ttcccattgtg gtcctctgac attgtcaactg gggaaaagaa tgaaccagt 1500
aagcctctgc agcccataat ccaaagaacaa aagccaaagg accagagtct tgccctgtcg 1560
cccaagctgg agtgcagtgg cacaatctt gctcacagca acctccgcct cctgggttca 1620
agtatttctc cagccctcagc ctcccgagta gctgggattt caggcgtgtg ccaccacgcc 1680
caggatcaag ttgcgttgcg atgtattata gaaaaacagg gcagaatcca cccagattta 1740
cagccacaca actctgggtc tgaaccttcc ctgtctcgac agcgacggca aaagaggaga 1800
gaacagactg agcacagagg gaaaaagaga caggtccgca gagatctt tgctttccaa 1860
gagtcgcctc ctgcattttt gccttctcat cccattgtt gggaaagtggta tgcacatca 1920
acacaaaaag aggctgaaaa ccaacgtaga gtggtcactg ggtctgtgag cagttcaagg 1980

agcagtgaga tgtcatcatc aaaggatcga ccattatcag ccagagagag gaggcgacta 2040
 aagcagtac aggaagaaaat gtcctctca ggccttcag tgagggaaagc gtctctgagt 2100
 gtagcagggc cagaaaaacc ccaggaagaa gaccagccct tgcctgccc acggctctcc 2160
 tctgactgca gcgtcactca ggaaaggaaa cagattcatt gtctgtctga ggatgagtt 2220
 agttcttcta caagttcaac tgataagtca gatggggatt acgggaaagg gaaaggttag 2280
 acaaatgaaa ttaatgcctt ggtacaattt atgactcaga ccctgaaaact ggattctaaa 2340
 gagagctgtg aagatgtccc ggtagcaaac ccagtgttag aattcaaaact tcatcgaaa 2400
 tatacgggaca cactgatact tcatggaaag gttgcagaag aggagagaa aatccatttt 2460
 aaagagctac cttcagctat tatgccagg tctgaaaaga tcaggagact agttgaagtc 2520
 ttgagaactg atgtaattcg tggcctggg gttcagctt tagagcagggt gtatgatctt 2580
 ttggaggagg aggtgaatt tgatagagag gtacgttgc gggagcacat gggtgaaaag 2640
 tatacaactt acagtgtgaa agctcgccag ttgaaatttt ttgaagaaaa catgaatttt 2700
 tgagcatttg tcctaattctg ctggcagaat taaagaccta ttttttagagg attttggctt 2760
 aaaaagcaag ggcaaacagt catttggaaag ccactcacca ctgtttata tctctttttt 2820
 atatctctt ggcgttccc tacagaaaag aaattggaca gaacagaata atatgaagca 2880
 ggatcacaaa agaaaaaaaaa ctttggctt catattctt ttgtgaggac aaatctgttg 2940
 tttgtttagt tactgtttac tgagccttaa tccaccaagt ttatatttag aattttattt 3000
 ttttaaggtt ctaattaact taaacacaga gctataaaat gctggattga aaattttata 3060
 ttgtaatgtt gagataaaag cagtaggaga aacaaatgac ataataatgtc gtcataattc 3120
 ctgctattgt taataaacctt aaggagtagt tgataaatta taaaattttt aaaaagtcaat 3180
 tcagttcttag aaatagattt aaagaatatg aagttctatc tagtacttga gcagctgtat 3240
 ttctttctt cacattgtg gacttttaat attttattct catttaatat aaacctcatc 3300
 tagggtatata acaaattaaa actgagacac attggctttg taaatcagta tgtttttaca 3360
 taatggttttt gtttagattt ttttccatc agtggaaaaca tttcttaagc acaaattttca 3420
 tttccattttt agcaattttgt aagcaagtc caggtccatt tagttttgg atatattttaa 3480
 tgtttgcctc ctgaagtttgc tcttcatgtt ctgtaaagata tttagttgtct ttccatgttt 3540
 taaaatgtatg attatatagc acatattttt tttagttgttt aataagaggt aataacccatc 3600
 taggaaagaa attttatgaa gttaaataca agtcttgaat agtacatttt cacttctgtt 3660
 ttcgagggac tctaaaaata aatattgtc cagaaa 3696

<210> 32
 <211> 841
 <212> PRT
 <213> Homo sapiens

<220>
 <223> serine threonine kinase 2 (STK2, NEK4)

<400> 32
 Met Pro Leu Ala Ala Tyr Cys Tyr Leu Arg Val Val Gly Lys Gly Ser
 1 5 10 15

Tyr Gly Glu Val Thr Leu Val Lys His Arg Arg Asp Gly Lys Gln Tyr
 20 25 30

Val Ile Lys Lys Leu Asn Leu Arg Asn Ala Ser Ser Arg Glu Arg Arg
 35 40 45

Ala Ala Glu Gln Glu Ala Gln Leu Leu Ser Gln Leu Lys His Pro Asn
 50 55 60

Ile Val Thr Tyr Lys Glu Ser Trp Glu Gly Asp Gly Leu Leu Tyr
 65 70 75 80

Ile Val Met Gly Phe Cys Glu Gly Asp Leu Tyr Arg Lys Leu Lys
 85 90 95

Glu Gln Lys Gly Gln Leu Leu Pro Glu Asn Gln Val Val Glu Trp Phe
 100 105 110

Val Gln Ile Ala Met Ala Leu Gln Tyr Leu His Glu Lys His Ile Leu
 115 120 125
 His Arg Asp Leu Lys Thr Gln Asn Val Phe Leu Thr Arg Thr Asn Ile
 130 135 140
 Ile Lys Val Gly Asp Leu Gly Ile Ala Arg Val Leu Glu Asn His Cys
 145 150 155 160
 Asp Met Ala Ser Thr Leu Ile Gly Thr Pro Tyr Tyr Met Ser Pro Glu
 165 170 175
 Leu Phe Ser Asn Lys Pro Tyr Asn Tyr Lys Ser Asp Val Trp Ala Leu
 180 185 190
 Gly Cys Cys Val Tyr Glu Met Ala Thr Leu Lys His Ala Phe Asn Ala
 195 200 205
 Lys Asp Met Asn Ser Leu Val Tyr Arg Ile Ile Glu Gly Lys Leu Pro
 210 215 220
 Pro Met Pro Arg Asp Tyr Ser Pro Glu Leu Ala Glu Leu Ile Arg Thr
 225 230 235 240
 Met Leu Ser Lys Arg Pro Glu Glu Arg Pro Ser Val Arg Ser Ile Leu
 245 250 255
 Arg Gln Pro Tyr Ile Lys Arg Gln Ile Ser Phe Phe Leu Glu Ala Thr
 260 265 270
 Lys Ile Lys Thr Ser Lys Asn Asn Ile Lys Asn Gly Asp Ser Gln Ser
 275 280 285
 Lys Pro Phe Ala Thr Val Val Ser Gly Glu Ala Glu Ser Asn His Glu
 290 295 300
 Val Ile His Pro Gln Pro Leu Ser Ser Glu Gly Ser Gln Thr Tyr Ile
 305 310 315 320
 Met Gly Glu Gly Lys Cys Leu Ser Gln Glu Lys Pro Arg Ala Ser Gly
 325 330 335
 Leu Leu Lys Ser Pro Ala Ser Leu Lys Ala His Thr Cys Lys Gln Asp
 340 345 350
 Leu Ser Asn Thr Thr Glu Leu Ala Thr Ile Ser Ser Val Asn Ile Asp
 355 360 365
 Ile Leu Pro Ala Lys Gly Arg Asp Ser Val Ser Asp Gly Phe Val Gln
 370 375 380
 Glu Asn Gln Pro Arg Tyr Leu Asp Ala Ser Asn Glu Leu Gly Gly Ile
 385 390 395 400
 Cys Ser Ile Ser Gln Val Glu Glu Met Leu Gln Asp Asn Thr Lys
 405 410 415
 Ser Ser Ala Gln Pro Glu Asn Leu Ile Pro Met Trp Ser Ser Asp Ile
 420 425 430

Val Thr Gly Glu Lys Asn Glu Pro Val Lys Pro Leu Gln Pro Leu Ile
 435 440 445
 Lys Glu Gln Lys Pro Lys Asp Gln Ser Leu Ala Leu Ser Pro Lys Leu
 450 455 460
 Glu Cys Ser Gly Thr Ile Leu Ala His Ser Asn Leu Arg Leu Leu Gly
 465 470 475 480
 Ser Ser Asp Ser Pro Ala Ser Ala Ser Arg Val Ala Gly Ile Thr Gly
 485 490 495
 Val Cys His His Ala Gln Asp Gln Val Ala Gly Glu Cys Ile Ile Glu
 500 505 510
 Lys Gln Gly Arg Ile His Pro Asp Leu Gln Pro His Asn Ser Gly Ser
 515 520 525
 Glu Pro Ser Leu Ser Arg Gln Arg Arg Gln Lys Arg Arg Glu Gln Thr
 530 535 540
 Glu His Arg Gly Glu Lys Arg Gln Val Arg Arg Asp Leu Phe Ala Phe
 545 550 555 560
 Gln Glu Ser Pro Pro Arg Phe Leu Pro Ser His Pro Ile Val Gly Lys
 565 570 575
 Val Asp Val Thr Ser Thr Gln Lys Glu Ala Glu Asn Gln Arg Arg Val
 580 585 590
 Val Thr Gly Ser Val Ser Ser Arg Ser Ser Glu Met Ser Ser Ser
 595 600 605
 Lys Asp Arg Pro Leu Ser Ala Arg Glu Arg Arg Arg Leu Lys Gln Ser
 610 615 620
 Gln Glu Glu Met Ser Ser Ser Gly Pro Ser Val Arg Lys Ala Ser Leu
 625 630 635 640
 Ser Val Ala Gly Pro Gly Lys Pro Gln Glu Glu Asp Gln Pro Leu Pro
 645 650 655
 Ala Arg Arg Leu Ser Ser Asp Cys Ser Val Thr Gln Glu Arg Lys Gln
 660 665 670
 Ile His Cys Leu Ser Glu Asp Glu Leu Ser Ser Ser Thr Ser Ser Thr
 675 680 685
 Asp Lys Ser Asp Gly Asp Tyr Gly Glu Gly Lys Gly Gln Thr Asn Glu
 690 695 700
 Ile Asn Ala Leu Val Gln Leu Met Thr Gln Thr Leu Lys Leu Asp Ser
 705 710 715 720
 Lys Glu Ser Cys Glu Asp Val Pro Val Ala Asn Pro Val Ser Glu Phe
 725 730 735
 Lys Leu His Arg Lys Tyr Arg Asp Thr Leu Ile Leu His Gly Lys Val
 740 745 750

Ala Glu Glu Ala Glu Glu Ile His Phe Lys Glu Leu Pro Ser Ala Ile
755 760 765

Met Pro Gly Ser Glu Lys Ile Arg Arg Leu Val Glu Val Leu Arg Thr
770 775 780

Asp Val Ile Arg Gly Leu Gly Val Gln Leu Leu Glu Gln Val Tyr Asp
785 790 795 800

Leu Leu Glu Glu Glu Asp Glu Phe Asp Arg Glu Val Arg Leu Arg Glu
805 810 815

His Met Gly Glu Lys Tyr Thr Thr Tyr Ser Val Lys Ala Arg Gln Leu
820 825 830

Lys Phe Phe Glu Glu Asn Met Asn Phe
835 840

```
<210> 33
<211> 1513
<212> DNA
<213> Homo sapiens
```

<220>
<223> serine threonine protein kinase NKIAMRE,
mitogen-activated protein kinase/cyclin-dependent
kinase-related protein kinase NKIATRE homologue

<210> 34
 <211> 455
 <212> PRT
 <213> Homo sapiens

<220>
 <223> serine threonine protein kinase NKIAMRE,
 mitogen-activated protein kinase/cyclin-dependent
 kinase-related protein kinase NKIATRE homologue

<400> 34
 Met Glu Met Tyr Glu Thr Leu Gly Lys Val Gly Glu Gly Ser Tyr Gly
 1 5 10 15

Thr Val Met Lys Cys Lys His Lys Asn Thr Gly Gln Ile Val Ala Ile
 20 25 30

Lys Ile Phe Tyr Glu Arg Pro Glu Gln Ser Val Asn Lys Ile Ala Met
 35 40 45

Arg Glu Ile Lys Phe Leu Lys Gln Phe His His Glu Asn Leu Val Asn
 50 55 60

Leu Ile Glu Val Phe Arg Gln Lys Lys Ile His Leu Val Phe Glu
 65 70 75 80

Phe Ile Asp His Thr Val Leu Asp Glu Leu Gln His Tyr Cys His Gly
 85 90 95

Leu Glu Ser Lys Arg Leu Arg Lys Tyr Leu Phe Gln Ile Leu Arg Ala
 100 105 110

Ile Asp Tyr Leu His Ser Asn Asn Ile Ile His Arg Asp Ile Lys Pro
 115 120 125

Glu Asn Ile Leu Val Ser Gln Ser Gly Ile Thr Lys Leu Cys Asp Phe
 130 135 140

Gly Phe Ala Arg Thr Leu Ala Ala Pro Gly Asp Ile Tyr Thr Asp Tyr
 145 150 155 160

Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Val Leu Lys Asp Thr
 165 170 175

Ser Tyr Gly Lys Pro Val Asp Ile Trp Ala Leu Gly Cys Met Ile Ile
 180 185 190

Glu Met Ala Thr Gly Asn Pro Tyr Leu Pro Ser Ser Ser Asp Leu Asp
 195 200 205

Leu Leu His Lys Ile Val Leu Lys Val Gly Asn Leu Ser Pro His Leu
 210 215 220

Gln Asn Ile Phe Ser Lys Ser Pro Ile Phe Ala Gly Val Val Leu Pro
 225 230 235 240

Gln Val Gln His Pro Lys Asn Ala Arg Lys Lys Tyr Pro Lys Leu Asn
 245 250 255

Gly Leu Leu Ala Asp Ile Val His Ala Cys Leu Gln Ile Asp Pro Ala
 260 265 270

Asp Arg Ile Ser Ser Ser Asp Leu Leu His His Glu Tyr Phe Thr Arg
275 280 285

Asp Gly Phe Ile Glu Lys Phe Met Pro Glu Leu Lys Ala Lys Leu Leu
290 295 300

Gin Glu Ala Lys Val Asn Ser Leu Ile Lys Pro Lys Glu Ser Ser Lys
305 310 315 320

Glu Asn Glu Leu Arg Lys Asp Glu Arg Lys Thr Val Tyr Thr Asn Thr
325 330 335

Leu Leu Ser Ser Ser Val Leu Gly Glu Glu Ile Glu Lys Glu Lys Lys
340 345 350

Pro Lys Glu Ile Lys Val Arg Val Ile Lys Val Lys Gly Gly Arg Gly
355 360 365

Asp Ile Ser Glu Pro Lys Lys Lys Glu Tyr Glu Gly Gly Leu Gly Gln
370 375 380

Gln Asp Ala Asn Glu Asn Val His Pro Met Ser Pro Asp Thr Lys Leu
385 390 395 400

Val Thr Ile Glu Pro Pro Asn Pro Ile Asn Pro Ser Thr Asn Cys Asn
405 410 415

Gly Leu Lys Glu Asn Pro His Cys Gly Ser Val Thr Met Pro Pro
420 425 430

Ile Asn Leu Thr Asn Ser Asn Leu Met Ala Ala Asn Leu Ser Ser Asn
435 440 445

Leu Phe His Pro Ser Val Arg
450 455

<210> 35

<211> 3504

<212> DNA

<213> Homo sapiens

<220>

<223> HBO1 histone acetyltransferase, MYST histone
acetyltransferase 2 (MYST2)

<400> 35

ggcgctgccc gaatcggaac cgtcggcccg cagccgcccgg caatgccgcg aaggaagagg 60
aatgcaggca gtagttcaga tggAACGAA gattccgatt tttctacaga tctcgagcac 120
acagacagtt cagaaagtga tggcacatcc cgacgatctg ctcgagtcac ccgctcctca 180
gccaggctaa gccagagtcc tcaagattcc agtccgttcc gaaatctgca gtcttttgc 240
actgaggagc ctgcttactc taccagaaga gtgaccggta gtcagcagca gcctacccca 300
gtgacaccga aaaaataaccc tcttcggcag actcgttcat ctggttcaga aactgagcaa 360
gtggttgatt tttcagatag agaaaactaaa aatacagctg atcatgatga gtcaccgcct 420
cgaactccaa ctggaaatgc gccttcttct gagtctgaca tagatatctc cagccccaaat 480
gtatctcacg atgagagcat tgccaaggac atgtccctga aggactcagg cagtgatctc 540
tctcatcgcc ccaagcgccg tcgcttccat gaaagctaca acttcaaatat gaagtgtcct 600
acaccaggct gtaactctct aggacacatt acaggaaaaac atgagagaca tttctccatc 660
tcaggatgcc cactgtatca taacctctca gctgacgaaat gcaagggtgag agcacagagc 720
cgggataagc agatagaaga aaggatgctg tctcacagggc aagatgacaa caacaggcat 780
gcaaccagggc accaggcacc aacggagagg cagttcgtat ataaggaaaa agtggctgaa 840

ctcaggaaga aaagaaaattc tggactgagc aaagaacaga aagagaaaata tatggaacac 900
 agacagacact atggaaacac acggaaacct ctttagaaa acctgacaag cgagtatgac 960
 ttggatctt tccgaagagc acaagccgg gcttcagagg atttggagaa gttaggctg 1020
 caaggccaaa tcacagaggg aagcaacatg attaaaacaa ttgccttgg ccgctatgag 1080
 cttgataacct ggtatcattc tccatatactt gaagaatatg cacggctggg acgtcttat 1140
 atgtgtgaat tctgtttaaa atatatgaag agccaaacga tactccgccc gcacatggcc 1200
 aaatgtgtg ggaacacccc acctgggtat gagatatact gcaaaggttc aatctctgtg 1260
 tttgaagtgg atggcaagaa aaacaagatc tactgcaaaa acctgtgcct gttggccaaa 1320
 cttttctgg accacaagac attatattat gatgtggagc ctttcctgtt ctatgttatg 1380
 acagaggccgg acaacactgg ctgtcacctg attggatatt tttctaagga aaagaattca 1440
 ttccctcaact acaacgtctc ctgtatcctt actatgcctc agtacatgag acagggctat 1500
 ggcaagatgc ttattgtt cagttatttgc cttccaaag tcgaagaaaa agttggctcc 1560
 ccagaacgtc cactctcaga tctggggctt ataagctatc gcagttactg gaaagaagta 1620
 cttctccgct acctgcataa ttttcaaggc aaagagatattt ctatcaaaga aatcagtcag 1680
 gagacggctg tgaatccgtt ggacattgtc agcaactgtc aagcccttca gatgctcaaa 1740
 tactggaagg gaaaacaccc agttttaaag agacaggacc tgattgtatg gtggatagcc 1800
 aaagaggccca aaaggtccaa ctccaataaa accatggatc ccagctgctt aaaaatggacc 1860
 cctcccaagg gcacttaaaag tgacctgtca ttccgagcca gcaacccca gcagtaggaa 1920
 tccgtaccct agggatctgt ctgtcatttc tctgttgctc ttgtgattgg caagtacagt 1980
 atcctttggg aaggccatcc ccctcaggac tgcaccatgc ctccaaatat ggctgccacc 2040
 agacgctggt tctgaggaac ttttgcgttgc gcctcagtga gttgcctgg atgggatctg 2100
 tattagactt gagtgcaggt ctctcagcac tgacccaaagg agttctgtt tggactgtta 2160
 cctgtccagt cactggttct ctctcatgt cctctcgccc catgaggttg tggactgtct 2220
 tctaagcgtg gtactagtgc ttgccacctg gtccaccatgc ctccaaatat ggctgccacc 2280
 accaggaccc ttccagttac tccttatatg ttttgcgttgc ggagggcag gaaaagggtg 2340
 gcacttgcgtt gttgtgtgg attggcaggg gttccattca ctttgggttca catcttgctt 2400
 taaaatttctt cattttgatt aagagaccc ttttgcgttgc gtattgggtt aaccagagcc 2460
 aaataactttt gaagagtttcc ccaaggacta gtcatggtaa tagcatataa ttgatctgaa 2520
 tgagatggag agaagaatga aggggtgggtt gttctgggtt tgatttgagt tcacctgtgg 2580
 gcagtgccca gttggcagtg tcttgggttca agggaaacggc tactacttt tgcctcaccc 2640
 taaaagtactc actagtaaat atttcccttct ctcttactc ccacttttta cgtttgcagg 2700
 tgccaaagta atgtccactt ttcccttca tgctgcataat taactggta attataactgc 2760
 agaaacctt tcacccac tagtctgata cagtagatct gtacttccat ataccttgc 2820
 ctgattttgt ctgagtgccc tgggagaagt agaaaatgtat gaaagtgc ttccgtatct 2880
 cagcccatga ctcagcaagg cagaatggcc accccctgcca aagtttgcctt ctctttcaa 2940
 cagtcctca ccctcccttca aggattaaag tgcttgcctt cttccacggaa ctccctcc 3000
 atttccctt tgggattttgt caccatcattt ctattctctt gtttttttattt tttgggtgtt 3060
 ttcaagtgaa ggaagagatg ttcccttcaaa ttctctcttca gcccattata acctgctatc 3120
 ttggggcaac ttttgcgttgc tgacatgtca cccttccaa cttggctctcc tccaaacatgc 3180
 tgtcttcatg tggagccctc accacaatcc ctgactccgg tcatttgc tttctcttgc 3240
 tcacactctgt acactactta tatttactgt ggggtgggg agctaatttt aagcatgttc 3300
 agtggcagct cccctccagt ttcaaggat ttatcaaaaaa gcaacttcac 3360
 taggggtttt cttaaggat aaaggccctt tacagaagct aaacccttcc ccacatgtgg 3420
 tagaatgtgc tcttctatataat cttactcataa ataaagcatg ttctctgttca aaaaaaaaaa 3480
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 3504

<210> 36
 <211> 611
 <212> PRT
 <213> Homo sapiens

<220>
 <223> HBO1 histone acetyltransferase, MYST histone
 acetyltransferase 2 (MYST2)

<400> 36
 Met Pro Arg Arg Lys Arg Asn Ala Gly Ser Ser Ser Asp Gly Thr Glu
 1 5 10 15

Asp Ser Asp Phe Ser Thr Asp Leu Glu His Thr Asp Ser Ser Glu Ser
 20 25 30

Asp Gly Thr Ser Arg Arg Ser Ala Arg Val Thr Arg Ser Ser Ala Arg
 35 40 45

Leu Ser Gln Ser Ser Gln Asp Ser Ser Pro Val Arg Asn Leu Gln Ser
 50 55 60

Phe Gly Thr Glu Glu Pro Ala Tyr Ser Thr Arg Arg Val Thr Arg Ser
 65 70 75 80

Gln Gln Gln Pro Thr Pro Val Thr Pro Lys Lys Tyr Pro Leu Arg Gln
 85 90 95

Thr Arg Ser Ser Gly Ser Glu Thr Glu Gln Val Val Asp Phe Ser Asp
 100 105 110

Arg Glu Thr Lys Asn Thr Ala Asp His Asp Glu Ser Pro Pro Arg Thr
 115 120 125

Pro Thr Gly Asn Ala Pro Ser Ser Glu Ser Asp Ile Asp Ile Ser Ser
 130 135 140

Pro Asn Val Ser His Asp Glu Ser Ile Ala Lys Asp Met Ser Leu Lys
 145 150 155 160

Asp Ser Gly Ser Asp Leu Ser His Arg Pro Lys Arg Arg Arg Phe His
 165 170 175

Glu Ser Tyr Asn Phe Asn Met Lys Cys Pro Thr Pro Gly Cys Asn Ser
 180 185 190

Leu Gly His Leu Thr Gly Lys His Glu Arg His Phe Ser Ile Ser Gly
 195 200 205

Cys Pro Leu Tyr His Asn Leu Ser Ala Asp Glu Cys Lys Val Arg Ala
 210 215 220

Gln Ser Arg Asp Lys Gln Ile Glu Glu Arg Met Leu Ser His Arg Gln
 225 230 235 240

Asp Asp Asn Asn Arg His Ala Thr Arg His Gln Ala Pro Thr Glu Arg
 245 250 255

Gln Leu Arg Tyr Lys Glu Lys Val Ala Glu Leu Arg Lys Lys Arg Asn
 260 265 270

Ser Gly Leu Ser Lys Glu Gln Lys Glu Lys Tyr Met Glu His Arg Gln
 275 280 285

Thr Tyr Gly Asn Thr Arg Glu Pro Leu Leu Glu Asn Leu Thr Ser Glu
 290 295 300

Tyr Asp Leu Asp Leu Phe Arg Arg Ala Gln Ala Arg Ala Ser Glu Asp
 305 310 315 320

Leu Glu Lys Leu Arg Leu Gln Gly Gln Ile Thr Glu Gly Ser Asn Met
 325 330 335

Ile Lys Thr Ile Ala Phe Gly Arg Tyr Glu Leu Asp Thr Trp Tyr His
 340 345 350
 Ser Pro Tyr Pro Glu Glu Tyr Ala Arg Leu Gly Arg Leu Tyr Met Cys
 355 360 365
 Glu Phe Cys Leu Lys Tyr Met Lys Ser Gln Thr Ile Leu Arg Arg His
 370 375 380
 Met Ala Lys Cys Val Trp Lys His Pro Pro Gly Asp Glu Ile Tyr Arg
 385 390 395 400
 Lys Gly Ser Ile Ser Val Phe Glu Val Asp Gly Lys Lys Asn Lys Ile
 405 410 415
 Tyr Cys Gln Asn Leu Cys Leu Leu Ala Lys Leu Phe Leu Asp His Lys
 420 425 430
 Thr Leu Tyr Tyr Asp Val Glu Pro Phe Leu Phe Tyr Val Met Thr Glu
 435 440 445
 Ala Asp Asn Thr Gly Cys His Leu Ile Gly Tyr Phe Ser Lys Glu Lys
 450 455 460
 Asn Ser Phe Leu Asn Tyr Asn Val Ser Cys Ile Leu Thr Met Pro Gln
 465 470 475 480
 Tyr Met Arg Gln Gly Tyr Gly Lys Met Leu Ile Asp Phe Ser Tyr Leu
 485 490 495
 Leu Ser Lys Val Glu Glu Lys Val Gly Ser Pro Glu Arg Pro Leu Ser
 500 505 510
 Asp Leu Gly Leu Ile Ser Tyr Arg Ser Tyr Trp Lys Glu Val Leu Leu
 515 520 525
 Arg Tyr Leu His Asn Phe Gln Gly Lys Glu Ile Ser Ile Lys Glu Ile
 530 535 540
 Ser Gln Glu Thr Ala Val Asn Pro Val Asp Ile Val Ser Thr Leu Gln
 545 550 555 560
 Ala Leu Gln Met Leu Lys Tyr Trp Lys Gly Lys His Leu Val Leu Lys
 565 570 575
 Arg Gln Asp Leu Ile Asp Glu Trp Ile Ala Lys Glu Ala Lys Arg Ser
 580 585 590
 Asn Ser Asn Lys Thr Met Asp Pro Ser Cys Leu Lys Trp Thr Pro Pro
 595 600 605
 Lys Gly Thr
 610

<210> 37
 <211> 21
 <212> DNA
 <213> Artificial Sequence

```

<220>
<223> Description of Artificial Sequence:CK2-specific
      siRNA molecule

<400> 37
aacattgaat tagatccacg t                                21

<210> 38
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PIM1-specific
      siRNA molecule

<400> 38
aaaactccga gtgaactggc c                                21

<210> 39
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HBO1-specific
      siRNA molecule

<400> 39
aactgagcaa gtgggttgcatt t                                21

<210> 40
<211> 409
<212> PRT
<213> Homo sapiens

<220>
<223> CDC7 cell division cycle 7 (CDC7), CDC7 cell
      division cycle 7-like 1 (CDC7L1) protein serine
      threonine kinase

<400> 40
Met Glu Ala Ser Leu Gly Ile Gln Met Asp Glu Pro Met Ala Phe Ser
  1           5           10           15

Pro Gln Arg Asp Arg Phe Gln Ala Glu Gly Ser Leu Lys Lys Asn Glu
  20           25           30

Gln Asn Phe Lys Leu Ala Gly Val Lys Lys Asp Ile Glu Lys Leu Tyr
  35           40           45

Glu Ala Val Pro Gln Leu Ser Asn Val Phe Lys Ile Glu Asp Lys Ile
  50           55           60

Gly Glu Gly Thr Phe Ser Ser Val Tyr Leu Ala Thr Ala Gln Leu Gln
  65           70           75           80

```

Val	Gly	Pro	Glu	Glu	Lys	Ile	Ala	Leu	Lys	His	Leu	Ile	Pro	Thr	Ser
85															95
His	Pro	Ile	Arg	Ile	Ala	Ala	Glu	Leu	Gln	Cys	Leu	Thr	Val	Ala	Gly
100															110
Gly	Gln	Asp	Asn	Val	Met	Gly	Val	Lys	Tyr	Cys	Phe	Arg	Lys	Asn	Asp
115															125
His	Val	Val	Ile	Ala	Met	Pro	Tyr	Leu	Glu	His	Glu	Ser	Phe	Leu	Asp
130															140
Ile	Leu	Asn	Ser	Leu	Ser	Phe	Gln	Glu	Val	Arg	Glu	Tyr	Met	Leu	Asn
145															160
Leu	Phe	Lys	Ala	Leu	Lys	Arg	Ile	His	Gln	Phe	Gly	Ile	Val	His	Arg
165															175
Asp	Val	Lys	Pro	Ser	Asn	Phe	Leu	Tyr	Asn	Arg	Arg	Leu	Lys	Lys	Tyr
180															190
Ala	Leu	Val	Asp	Phe	Gly	Leu	Ala	Gln	Gly	Thr	His	Asp	Thr	Lys	Ile
195															205
Glu	Leu	Leu	Lys	Phe	Val	Gln	Ser	Glu	Ala	Gln	Glu	Arg	Cys	Ser	
210															
215															220
Gln	Asn	Lys	Ser	His	Ile	Ile	Thr	Gly	Asn	Lys	Ile	Pro	Leu	Ser	Gly
225															240
Pro	Val	Pro	Lys	Glu	Leu	Asp	Gln	Gln	Ser	Thr	Thr	Lys	Ala	Ser	Val
245															255
Lys	Arg	Pro	Tyr	Thr	Asn	Ala	Gln	Ile	Gln	Ile	Lys	Gln	Gly	Lys	Asp
260															270
Gly	Lys	Glu	Gly	Ser	Val	Gly	Leu	Ser	Val	Gln	Arg	Ser	Val	Phe	Gly
275															285
Glu	Arg	Asn	Phe	Asn	Ile	His	Ser	Ser	Ile	Ser	His	Glu	Ser	Pro	Ala
290															300
Val	Lys	Leu	Met	Lys	Gln	Ser	Lys	Thr	Val	Asp	Val	Leu	Ser	Arg	Lys
305															320
310															
Leu	Ala	Thr	Lys	Lys	Ala	Ile	Ser	Thr	Lys	Val	Met	Asn	Ser	Ala	
325															335
Val	Met	Arg	Lys	Thr	Ala	Ser	Ser	Cys	Pro	Ala	Ser	Leu	Thr	Cys	Asp
340															350
Cys	Tyr	Ala	Thr	Asp	Lys	Val	Cys	Ser	Ile	Cys	Leu	Ser	Arg	Arg	Gln
355															365
Gln	Val	Ala	Pro	Arg	Ala	Gly	Thr	Pro	Gly	Phe	Arg	Ala	Pro	Glu	Val
370															380

Leu Thr Lys Cys Pro Asn Gln Thr Thr Ala Ile Asp Met Trp Ser Ala
385 390 395 400

Gly Val Ile Phe Leu Ser Leu Leu Ser
405

<210> 41
<211> 314
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<223> CDC7

<400> 41
Met Thr Ser Lys Thr Lys Asn Ile Asp Asp Ile Pro Pro Glu Ile Lys
1 5 10 15

Glu Glu Met Ile Gln Leu Tyr His Asp Leu Pro Gly Ile Glu Asn Glu
20 25 30

Tyr Lys Leu Ile Asp Lys Ile Gly Glu Gly Thr Phe Ser Ser Val Tyr
35 40 45

Lys Ala Lys Asp Ile Thr Gly Lys Ile Thr Lys Lys Phe Ala Ser His
50 55 60

Phe Trp Asn Tyr Gly Ser Asn Tyr Val Ala Leu Lys Lys Ile Tyr Val
65 70 75 80

Thr Ser Ser Pro Gln Arg Ile Tyr Asn Glu Leu Asn Leu Leu Tyr Ile
85 90 95

Met Thr Gly Ser Ser Arg Val Ala Pro Leu Cys Asp Ala Lys Arg Val
100 105 110

Arg Asp Gln Val Ile Ala Val Leu Pro Tyr Tyr Pro His Glu Glu Phe
115 120 125

Arg Thr Phe Tyr Arg Asp Leu Pro Ile Lys Gly Ile Lys Lys Tyr Ile
130 135 140

Trp Glu Leu Leu Arg Ala Leu Lys Phe Val His Ser Lys Gly Ile Ile
145 150 155 160

His Arg Asp Ile Lys Pro Thr Asn Phe Leu Phe Asn Leu Glu Leu Gly
165 170 175

Arg Gly Val Leu Val Asp Phe Gly Leu Ala Glu Ala Gln Met Asp Tyr
180 185 190

Lys Ser Met Ile Ser Ser Gln Asn Asp Tyr Asp Asn Tyr Ala Asn Thr
195 200 205

Asn His Asp Gly Gly Tyr Ser Met Arg Asn His Glu Gln Phe Cys Pro
210 215 220

Cys Ile Met Arg Asn Gln Tyr Ser Pro Asn Ser His Asn Gln Thr Pro
225 230 235 240

Pro Met Val Thr Ile Gln Asn Gly Lys Val Val His Leu Asn Asn Val
 245 250 255
 Asn Gly Val Asp Leu Thr Lys Gly Tyr Pro Lys Asn Glu Thr Arg Arg
 260 265 270
 Ile Lys Arg Ala Asn Arg Ala Gly Thr Arg Gly Phe Arg Ala Pro Glu
 275 280 285
 Val Leu Met Lys Cys Gly Ala Gln Ser Thr Lys Ile Asp Ile Trp Ser
 290 295 300
 Val Gly Val Ile Leu Leu Ser Leu Leu Gly
 305 310

<210> 42
 <211> 294
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:protein kinase
 consensus sequence

<400> 42
 Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
 1 5 10 15
 Lys Ala Lys His Lys Asp Lys Thr Gly Lys Ile Val Ala Val Lys Ile
 20 25 30
 Leu Lys Lys Glu Lys Glu Ser Ile Lys Glu Lys Arg Phe Leu Arg Glu
 35 40 45
 Ile Gln Ile Leu Lys Arg Leu Ser His Pro Asn Ile Val Arg Leu Ile
 50 55 60
 Gly Val Phe Glu Asp Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr
 65 70 75 80
 Met Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Gly Pro
 85 90 95
 Leu Ser Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly
 100 105 110
 Leu Glu Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro
 115 120 125
 Glu Asn Ile Leu Leu Asp Glu Asn Asp Gly Thr Val Lys Ile Ala Asp
 130 135 140
 Phe Gly Leu Ala Arg Leu Leu Glu Ser Ser Ser Lys Leu Thr Thr Phe
 145 150 155 160
 Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile Leu Glu Gly
 165 170 175
 Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly Val Ile Leu
 180 185 190

Tyr	Glu	Leu	Leu	Thr	Gly	Gly	Pro	Leu	Phe	Pro	Gly	Ala	Asp	Leu	Pro
195							200					205			
Ala	Phe	Thr	Gly	Gly	Asp	Glu	Val	Asp	Gln	Leu	Ile	Ile	Phe	Val	Leu
210						215					220				
Lys	Leu	Pro	Phe	Ser	Asp	Glu	Leu	Pro	Lys	Thr	Arg	Ile	Asp	Pro	Leu
225						230			235			240			
Glu	Glu	Leu	Phe	Arg	Ile	Ile	Lys	Arg	Pro	Gly	Leu	Arg	Leu	Pro	Leu
					245			250			255				
Pro	Ser	Asn	Cys	Ser	Glu	Glu	Leu	Lys	Asp	Leu	Leu	Lys	Lys	Cys	Leu
					260			265			270				
Asn	Lys	Asp	Pro	Ser	Lys	Arg	Pro	Gly	Ser	Ala	Thr	Ala	Lys	Glu	Ile
					275			280			285				
Leu	Asn	His	Pro	Trp	Phe										
					290										

<210> 43

<211> 253

<212> PRT

<213> Homo sapiens

<220>

<223> cytokine-inducible kinase (CNK) serine threonine kinase, proliferation-related kinase (PRK), polo-like kinase 3 (PLK3)

<400> 43

Tyr	Leu	Lys	Gly	Arg	Leu	Leu	Gly	Lys	Gly	Gly	Phe	Ala	Arg	Cys	Tyr
1					5				10				15		

Glu	Ala	Thr	Asp	Thr	Glu	Thr	Gly	Ser	Ala	Tyr	Ala	Val	Lys	Val	Ile
					20				25				30		

Pro	Gln	Ser	Arg	Val	Ala	Lys	Pro	His	Gln	Arg	Glu	Lys	Ile	Leu	Asn
					35			40			45				

Glu	Ile	Glu	Leu	His	Arg	Asp	Leu	Gln	His	Arg	His	Ile	Val	Arg	Phe
					50			55			60				

Ser	His	His	Phe	Glu	Asp	Ala	Asp	Asn	Ile	Tyr	Ile	Phe	Leu	Glu	Leu
					65			70			75			80	

Cys	Ser	Arg	Lys	Ser	Leu	Ala	His	Ile	Trp	Lys	Ala	Arg	His	Thr	Leu
					85				90			95			

Leu	Glu	Pro	Glu	Val	Arg	Tyr	Tyr	Leu	Arg	Gln	Ile	Leu	Ser	Gly	Leu
					100			105			110				

Lys	Tyr	Leu	His	Gln	Arg	Gly	Ile	Leu	His	Arg	Asp	Leu	Lys	Leu	Gly
					115			120			125				

Asn	Phe	Phe	Ile	Thr	Glu	Asn	Met	Glu	Leu	Lys	Val	Gly	Asp	Phe	Gly
					130			135			140				

Leu Ala Ala Arg Leu Glu Pro Pro Glu Gln Arg Lys Lys Thr Ile Cys
145 150 155 160

Gly Thr Pro Asn Tyr Val Ala Pro Glu Val Leu Leu Arg Gln Gly His
165 170 175

Gly Pro Glu Ala Asp Val Trp Ser Leu Gly Cys Val Met Tyr Thr Leu
180 185 190

Leu Cys Gly Ser Pro Pro Phe Glu Thr Ala Asp Leu Lys Glu Thr Tyr
195 200 205

Arg Cys Ile Lys Gln Val His Tyr Thr Leu Pro Ala Ser Leu Ser Leu
210 215 220

Pro Ala Arg Gln Leu Leu Ala Ala Ile Leu Arg Ala Ser Pro Arg Asp
225 230 235 240

Arg Pro Ser Ile Asp Gln Ile Leu Arg His Asp Phe Phe
245 250

<210> 44

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
peptide

<400> 44

His Arg Asp Leu Lys
1 5

<210> 45

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
peptide

<400> 45

Asp Phe Gly Leu Ala
1 5

<210> 46

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
peptide

<400> 46
Ala Pro Glu Val
1

<210> 47
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 47
Asp Val Trp Ser Leu Gly
1 5

<210> 48
<211> 256
<212> PRT
<213> Homo sapiens

<220>
<223> serine threonine kinase 2 (STK2, NEK4)

<400> 48
Tyr Cys Tyr Leu Arg Val Val Gly Lys Gly Ser Tyr Gly Glu Val Thr
1 5 10 15

Leu Val Lys His Arg Arg Asp Gly Lys Gln Tyr Val Ile Lys Lys Leu
20 25 30

Asn Leu Arg Asn Ala Ser Ser Arg Glu Arg Arg Ala Ala Glu Gln Glu
35 40 45

Ala Gln Leu Leu Ser Gln Leu Lys His Pro Asn Ile Val Thr Tyr Lys
50 55 60

Glu Ser Trp Glu Gly Gly Asp Gly Leu Leu Tyr Ile Val Met Gly Phe
65 70 75 80

Cys Glu Gly Gly Asp Leu Tyr Arg Lys Leu Lys Glu Gln Lys Gly Gln
85 90 95

Leu Leu Pro Glu Asn Gln Val Val Glu Trp Phe Val Gln Ile Ala Met
100 105 110

Ala Leu Gln Tyr Leu His Glu Lys His Ile Leu His Arg Asp Leu Lys
115 120 125

Thr Gln Asn Val Phe Leu Thr Arg Thr Asn Ile Ile Lys Val Gly Asp
130 135 140

Leu Gly Ile Ala Arg Val Leu Glu Asn His Cys Asp Met Ala Ser Thr
145 150 155 160

Leu Ile Gly Thr Pro Tyr Tyr Met Ser Pro Glu Leu Phe Ser Asn Lys
165 170 175

Pro Tyr Asn Tyr Lys Ser Asp Val Trp Ala Leu Gly Cys Cys Val Tyr
180 185 190

Glu Met Ala Thr Leu Lys His Ala Phe Asn Ala Lys Asp Met Asn Ser
195 200 205

Leu Val Tyr Arg Ile Ile Glu Gly Lys Leu Pro Pro Met Pro Arg Asp
210 215 220

Tyr Ser Pro Glu Leu Ala Glu Leu Ile Arg Thr Met Leu Ser Lys Arg
225 230 235 240

Pro Glu Glu Arg Pro Ser Val Arg Ser Ile Leu Arg Gln Pro Tyr Ile
245 250 255

<210> 49

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
peptide

<400> 49

His Pro Asn Ile Val
1 5

<210> 50

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
peptide

<400> 50

Glu Gly Gly Asp Leu
1 5

<210> 51

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:protein kinase
consensus sequence

<400> 51

Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
1 5 10 15

Lys Ala Lys His Lys Asp Lys Thr Gly Lys Ile Val Ala Val Lys Ile
20 25 30

Leu	Lys	Lys	Glu	Lys	Glu	Ser	Ile	Lys	Glu	Lys	Arg	Phe	Leu	Arg	Glu
35							40							45	
Ile	Gln	Ile	Leu	Lys	Arg	Leu	Ser	His	Pro	Asn	Ile	Val	Arg	Leu	Ile
50							55					60			
Gly	Val	Phe	Glu	Asp	Thr	Asp	Asp	His	Leu	Tyr	Leu	Val	Met	Glu	Tyr
65							70					75		80	
Met	Glu	Gly	Gly	Asp	Leu	Phe	Asp	Tyr	Leu	Arg	Arg	Asn	Gly	Gly	Pro
	85							90					95		
Leu	Ser	Glu	Lys	Glu	Ala	Lys	Lys	Ile	Ala	Leu	Gln	Ile	Leu	Arg	Gly
	100							105					110		
Leu	Glu	Tyr	Leu	His	Ser	Asn	Gly	Ile	Val	His	Arg	Asp	Leu	Lys	Pro
	115						120					125			
Glu	Asn	Ile	Leu	Leu	Asp	Glu	Asn	Asp	Gly	Thr	Val	Lys	Ile	Ala	Asp
	130						135					140			
Phe	Gly	Leu	Ala	Arg	Leu	Leu	Glu	Ser	Ser	Ser	Lys	Leu	Thr	Thr	Phe
	145						150					155			160
Val	Gly	Thr	Pro	Trp	Tyr	Met	Met	Ala	Pro	Glu	Val	Ile	Leu	Glu	Gly
	165							170					175		
Arg	Gly	Tyr	Ser	Ser	Lys	Val	Asp	Val	Trp	Ser	Leu	Gly	Val	Ile	Leu
	180							185					190		
Tyr	Glu	Leu	Leu	Thr	Gly	Gly	Pro	Leu	Phe	Pro	Gly	Ala	Asp	Leu	Pro
	195							200					205		
Ala	Phe	Thr	Gly	Gly	Asp	Glu	Val	Asp	Gln	Leu	Ile	Ile	Phe	Val	Leu
	210						215					220			
Lys	Leu	Pro	Phe	Ser	Asp	Glu	Leu	Pro	Lys	Thr	Arg	Ile	Asp	Pro	Leu
	225						230					235			240
Glu	Glu	Leu	Phe	Arg	Ile	Ile	Lys	Arg	Pro	Gly	Leu	Arg	Leu	Pro	Leu
	245							250					255		
Pro	Ser	Asn	Cys	Ser	Glu	Glu	Leu	Lys	Asp	Leu	Leu	Lys	Lys	Cys	Leu
	260							265					270		
Asn	Lys	Asp	Pro	Ser	Lys	Arg	Pro	Gly	Ser	Ala	Thr	Ala	Lys	Glu	Ile
	275						280					285			
Leu	Asn	His	Pro	Trp	Phe										
	290														

<210> 52
<211> 286
<212> PRT
<213> Homo sapiens

<220>
<223> serine threonine protein kinase casein kinase 2,
alpha 1 subunit isoform a, transcript variant 2
(CK2, CK2alpha), CK2 catalytic subunit alpha

<400> 52
 Tyr Gln Leu Val Arg Lys Leu Gly Arg Gly Lys Tyr Ser Glu Val Phe
 1 5 10 15
 Glu Ala Ile Asn Ile Thr Asn Asn Glu Lys Val Val Val Lys Ile Leu
 20 25 30
 Lys Pro Val Lys Lys Lys Ile Lys Arg Glu Ile Lys Ile Leu Glu
 35 40 45
 Asn Leu Arg Gly Gly Pro Asn Ile Ile Thr Leu Ala Asp Ile Val Lys
 50 55 60
 Asp Pro Val Ser Arg Thr Pro Ala Leu Val Phe Glu His Val Asn Asn
 65 70 75 80
 Thr Asp Phe Lys Gln Leu Tyr Gln Thr Leu Thr Asp Tyr Asp Ile Arg
 85 90 95
 Phe Tyr Met Tyr Glu Ile Leu Lys Ala Leu Asp Tyr Cys His Ser Met
 100 105 110
 Gly Ile Met His Arg Asp Val Lys Pro His Asn Val Met Ile Asp His
 115 120 125
 Glu His Arg Lys Leu Arg Leu Ile Asp Trp Gly Leu Ala Glu Phe Tyr
 130 135 140
 His Pro Gly Gln Glu Tyr Asn Val Arg Val Ala Ser Arg Tyr Phe Lys
 145 150 155 160
 Gly Pro Glu Leu Leu Val Asp Tyr Gln Met Tyr Asp Tyr Ser Leu Asp
 165 170 175
 Met Trp Ser Leu Gly Cys Met Leu Ala Ser Met Ile Phe Arg Lys Glu
 180 185 190
 Pro Phe Phe His Gly His Asp Asn Tyr Asp Gln Leu Val Arg Ile Ala
 195 200 205
 Lys Val Leu Gly Thr Glu Asp Leu Tyr Asp Tyr Ile Asp Lys Tyr Asn
 210 215 220
 Ile Glu Leu Asp Pro Arg Phe Asn Asp Ile Leu Gly Arg His Ser Arg
 225 230 235 240
 Lys Arg Trp Glu Arg Phe Val His Ser Glu Asn Gln His Leu Val Ser
 245 250 255
 Pro Glu Ala Leu Asp Phe Leu Asp Lys Leu Leu Arg Tyr Asp His Gln
 260 265 270
 Ser Arg Leu Thr Ala Arg Glu Ala Met Glu His Pro Tyr Phe
 275 280 285

<210> 53
 <211> 5
 <212> PRT
 <213> Artificial Sequence

```

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 53
Val Lys Ile Leu Lys
 1           5

<210> 54
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 54
Trp Ser Leu Gly
 1

<210> 55
<211> 298
<212> PRT
<213> Homo sapiens

<220>
<223> cyclin-dependent kinase 2 (CDK2)

<400> 55
Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly
 1           5           10           15

Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu
 20          25           30

Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala
 35          40           45

Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val
 50          55           60

Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe
 65          70           75           80

Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu
 85          90           95

Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu
100          105          110

Gln Gly Leu Ala Phe Cys His Ser His Arg Val Leu His Arg Asp Leu
115          120          125

Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu Gly Ala Ile Lys Leu Ala
130          135          140

Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Val Arg Thr Tyr Thr
145          150          155          160

```

His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	Leu	Gly
				165				170						175	
Cys	Lys	Tyr	Tyr	Ser	Thr	Ala	Val	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Ile
				180				185						190	
Phe	Ala	Glu	Met	Val	Thr	Arg	Arg	Ala	Leu	Phe	Pro	Gly	Asp	Ser	Glu
				195				200					205		
Ile	Asp	Gln	Leu	Phe	Arg	Ile	Phe	Arg	Thr	Leu	Gly	Thr	Pro	Asp	Glu
				210				215				220			
Val	Val	Trp	Pro	Gly	Val	Thr	Ser	Met	Pro	Asp	Tyr	Lys	Pro	Ser	Phe
				225				230			235			240	
Pro	Lys	Trp	Ala	Arg	Gln	Asp	Phe	Ser	Lys	Val	Val	Pro	Pro	Leu	Asp
				245				250					255		
Glu	Asp	Gly	Arg	Ser	Leu	Leu	Ser	Gln	Met	Leu	His	Tyr	Asp	Pro	Asn
				260				265				270			
Lys	Arg	Ile	Ser	Ala	Lys	Ala	Ala	Leu	Ala	His	Pro	Phe	Phe	Gln	Asp
				275				280				285			
Val	Thr	Lys	Pro	Val	Pro	His	Leu	Arg	Leu						
				290			295								

<210> 56
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Xeroderma
 pigmentosum complementation group XPG N-terminal
 domain (XPG_N) consensus sequence

<400> 56															
Met	Gly	Ile	Lys	Gly	Leu	Leu	Pro	Ile	Leu	Lys	Pro	Val	Ala	Pro	Glu
1					5				10					15	
Ala	Ile	Arg	Ser	Val	Ser	Ile	Glu	Ala	Leu	Glu	Gly	Tyr	Tyr	Lys	Val
									25					30	
Leu	Ala	Ile	Asp	Ala	Ser	Ile	Trp	Leu	Tyr	Gln	Phe	Leu	Lys	Ala	Val
								35			40		45		
Arg	Asp	Gln	Leu	Gly	Asn	Asn	Leu	Glu	Asn	Glu	Glu	Gly	Glu	Thr	Thr
								50			55		60		
Ser	His	Leu	Met	Gly	Leu	Phe	Ser	Arg	Leu	Cys	Arg	Leu	Leu	Asp	Phe
								65			70		75		80
Gly	Ile	Lys	Pro	Ile	Phe	Val	Phe	Asp	Gly	Gly	Ala	Pro	Asn	Asp	Leu
								85			90		95		
Lys	Ala	Glu	Thr	Leu	Gln	Lys	Arg	Ser	Ala	Arg	Arg	Gln	Glu	Ala	
								100			105		110		

```

<210> 57
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> flap structure-specific endonuclease 1 (FEN1)
      5'-3' exonuclease

<400> 57
Met Gly Ile Gln Gly Leu Ala Lys Leu Ile Ala Asp Val Ala Pro Ser
 1           5           10           15

Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
 20           25           30

Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
 35           40           45

Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
 50           55           60

Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
 65           70           75           80

Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu
 85           90           95

Leu Ala Lys Arg Ser Glu Arg Arg Ala Glu Ala
 100          105

<210> 58
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 58
Ala Ile Asp Ala Ser
 1           5

<210> 59
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 59
Tyr Gln Phe Leu
 1

```

```

<210> 60
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 60
Asn Glu Glu Gly Glu Thr Thr Ser His Leu Met Gly
      1           5           10

<210> 61
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 61
Gly Ile Lys Pro
      1

<210> 62
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 62
Val Phe Asp Gly
      1

<210> 63
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Xeroderma
      pigmentosum complementation group XPG I-region
      domain (XPG_I) consensus sequence

<400> 63
Arg Leu Met Gly Ile Pro Tyr Ile Val Ala Pro Gly Val Glu Ala Glu
      1           5           10           15

Ala Gln Cys Ala Tyr Leu Glu Lys Lys Gly Leu Val Asp Gly Ile Ile
      20          25           30

Thr Glu Asp Ser Asp Val Leu Leu Phe Gly Ala Pro Arg Leu Leu Arg
      35          40           45

```

Asn Leu Thr Leu Ser Gly Lys Lys Ser Gly Pro Ser Ile Thr Ser Leu
50 55 60

Lys Val Glu Ile Glu Glu Ile Asp Leu Glu Ser Leu Leu Arg Glu Leu
65 70 75 80

Gly Leu Gly Lys Leu Ser Arg Glu Gln Leu Ile Asp Leu Ala Ile Leu
85 90 95

Leu Gly Cys Asp Tyr Thr Glu Gly
100

<210> 64
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<223> flap structure-specific endonuclease 1 (FEN1)
5'-3' exonuclease

<400> 64
Ser Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu Ala
1 5 10 15

Ser Cys Ala Ala Leu Val Lys Ala Gly Lys Val Tyr Ala Ala Ala Thr
20 25 30

Glu Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg His
35 40 45

Leu Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His Leu
50 55 60

Ser Arg Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val Asp
65 70 75 80

Leu Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser
85 90

<210> 65
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 65
Leu Met Gly Ile Pro Tyr
1 5

<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence

```

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 66
Glu Ala Glu Ala
 1

<210> 67
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 67
Glu Leu Gly Leu
 1

<210> 68
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 68
Ile Leu Leu Gly
 1

<210> 69
<211> 261
<212> PRT
<213> Homo sapiens

<220>
<223> HBO1 histone acetyltransferase, MYST histone
      acetyltransferase 2 (MYST2)

<400> 69
Tyr His Ser Pro Tyr Pro Glu Glu Tyr Ala Arg Leu Gly Arg Leu Tyr
 1           5           10          15

Met Cys Glu Phe Cys Leu Lys Tyr Met Lys Ser Gln Thr Ile Leu Arg
 20           25           30

Arg His Met Ala Lys Cys Val Trp Lys His Pro Pro Gly Asp Glu Ile
 35           40           45

Tyr Arg Lys Gly Ser Ile Ser Val Phe Glu Val Asp Gly Lys Lys Asn
 50           55           60

Lys Ile Tyr Cys Gln Asn Leu Cys Leu Leu Ala Lys Leu Phe Leu Asp
 65           70           75           80

```

His	Lys	Thr	Leu	Tyr	Tyr	Asp	Val	Glu	Pro	Phe	Leu	Phe	Tyr	Val	Met
									85						95
Thr	Glu	Ala	Asp	Asn	Thr	Gly	Cys	His	Leu	Ile	Gly	Tyr	Phe	Ser	Lys
									100						110
Glu	Lys	Asn	Ser	Phe	Leu	Asn	Tyr	Asn	Val	Ser	Cys	Ile	Leu	Thr	Met
									115						125
Pro	Gln	Tyr	Met	Arg	Gln	Gly	Tyr	Gly	Lys	Met	Leu	Ile	Asp	Phe	Ser
									130						140
Tyr	Leu	Leu	Ser	Lys	Val	Glu	Glu	Lys	Val	Gly	Ser	Pro	Glu	Arg	Pro
									145						160
Leu	Ser	Asp	Leu	Gly	Leu	Ile	Ser	Tyr	Arg	Ser	Tyr	Trp	Lys	Glu	Val
									165						175
Leu	Leu	Arg	Tyr	Leu	His	Asn	Phe	Gln	Gly	Lys	Glu	Ile	Ser	Ile	Lys
									180						190
Glu	Ile	Ser	Gln	Glu	Thr	Ala	Val	Asn	Pro	Val	Asp	Ile	Val	Ser	Thr
									195						205
Leu	Gln	Ala	Leu	Gln	Met	Leu	Lys	Tyr	Trp	Lys	Gly	Lys	His	Leu	Val
									210						220
Leu	Lys	Arg	Gln	Asp	Leu	Ile	Asp	Glu	Trp	Ile	Ala	Lys	Glu	Ala	Lys
									225						240
Arg	Ser	Asn	Ser	Asn	Lys	Thr	Met	Asp	Pro	Ser	Cys	Leu	Lys	Trp	Thr
									245						255
Pro	Pro	Lys	Gly	Thr											
									260						

<210> 70
 <211> 265
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <223> *Esa1*

<400> 70															
Tyr	Phe	Ser	Pro	Tyr	Pro	Ile	Glu	Leu	Thr	Asp	Glu	Asp	Phe	Ile	Tyr
1									10						15
Ile	Asp	Asp	Phe	Thr	Leu	Gln	Tyr	Phe	Gly	Ser	Lys	Lys	Gln	Tyr	Glu
									20						30
Arg	Tyr	Arg	Lys	Lys	Cys	Thr	Leu	Arg	His	Pro	Pro	Gly	Asn	Glu	Ile
									35						45
Tyr	Arg	Asp	Asp	Tyr	Val	Ser	Phe	Phe	Glu	Ile	Asp	Gly	Arg	Lys	Gln
									50						60
Arg	Thr	Trp	Cys	Arg	Asn	Leu	Cys	Leu	Leu	Ser	Lys	Leu	Phe	Leu	Asp
									65						80

His	Lys	Thr	Leu	Tyr	Tyr	Asp	Val	Asp	Pro	Phe	Leu	Phe	Tyr	Cys	Met
85									90					95	
Thr	Arg	Arg	Asp	Glu	Leu	Gly	His	His	Leu	Val	Gly	Tyr	Phe	Ser	Lys
100								105					110		
Glu	Lys	Glu	Ser	Ala	Asp	Gly	Tyr	Asn	Val	Ala	Cys	Ile	Leu	Thr	Leu
115								120				125			
Pro	Gln	Tyr	Gln	Arg	Met	Gly	Tyr	Gly	Lys	Leu	Leu	Ile	Glu	Phe	Ser
130					135					140					
Tyr	Glu	Leu	Ser	Lys	Lys	Glu	Asn	Lys	Val	Gly	Ser	Pro	Glu	Lys	Pro
145					150				155				160		
Leu	Ser	Asp	Leu	Gly	Leu	Leu	Ser	Tyr	Arg	Ala	Tyr	Trp	Ser	Asp	Thr
165								170					175		
Leu	Ile	Thr	Leu	Leu	Val	Glu	His	Gln	Lys	Glu	Ile	Thr	Ile	Asp	Glu
180								185					190		
Ile	Ser	Ser	Met	Thr	Ser	Met	Thr	Thr	Asp	Ile	Leu	His	Thr	Ala	
195						200						205			
Lys	Thr	Leu	Asn	Ile	Leu	Arg	Tyr	Tyr	Lys	Gly	Gln	His	Ile	Ile	Phe
210						215					220				
Leu	Asn	Glu	Asp	Ile	Leu	Asp	Arg	Tyr	Asn	Arg	Leu	Lys	Ala	Lys	Lys
225					230				235					240	
Arg	Arg	Thr	Ile	Asp	Pro	Asn	Arg	Leu	Ile	Trp	Lys	Pro	Pro	Val	Phe
245								250					255		
Thr	Ala	Ser	Gln	Leu	Arg	Phe	Ala	Trp							
260							265								

<210> 71
 <211> 253
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PIM1 oncogene serine threonine kinase

<400> 71
 Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly Phe Gly Ser Val Tyr
 1 5 10 15

Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val Ala Ile Lys His Val
 20 25 30

Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu Pro Asn Gly Thr Arg
 35 40 45

Val Pro Met Glu Val Val Leu Leu Lys Lys Val Ser Ser Gly Phe Ser
 50 55 60

Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg Pro Asp Ser Phe Val
 65 70 75 80

Leu	Ile	Leu	Glu	Arg	Pro	Glu	Pro	Val	Gln	Asp	Leu	Phe	Asp	Phe	Ile
					85				90						95
Thr	Glu	Arg	Gly	Ala	Leu	Gln	Glu	Glu	Leu	Ala	Arg	Ser	Phe	Phe	Trp
					100			105							110
Gln	Val	Leu	Glu	Ala	Val	Arg	His	Cys	His	Asn	Cys	Gly	Val	Leu	His
					115			120							125
Arg	Asp	Ile	Lys	Asp	Glu	Asn	Ile	Leu	Ile	Asp	Leu	Asn	Arg	Gly	Glu
					130			135							140
Leu	Lys	Leu	Ile	Asp	Phe	Gly	Ser	Gly	Ala	Leu	Leu	Lys	Asp	Thr	Val
					145			150			155				160
Tyr	Thr	Asp	Phe	Asp	Gly	Thr	Arg	Val	Tyr	Ser	Pro	Pro	Glu	Trp	Ile
					165			170							175
Arg	Tyr	His	Arg	Tyr	His	Gly	Arg	Ser	Ala	Ala	Val	Trp	Ser	Leu	Gly
					180			185							190
Ile	Leu	Leu	Tyr	Asp	Met	Val	Cys	Gly	Asp	Ile	Pro	Phe	Glu	His	Asp
					195			200							205
Glu	Glu	Ile	Ile	Arg	Gly	Gln	Val	Phe	Phe	Arg	Gln	Arg	Val	Ser	Ser
					210			215							220
Glu	Cys	Gln	His	Leu	Ile	Arg	Trp	Cys	Leu	Ala	Leu	Arg	Pro	Ser	Asp
					225			230			235				240
Arg	Pro	Thr	Phe	Glu	Glu	Ile	Gln	Asn	His	Pro	Trp	Met			
					245			250							

<210> 72

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus peptide

<400> 72

Asp Leu Phe Asp

1

<210> 73

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus peptide

<400> 73

Glu Asn Ile Leu

1

```

<210> 74
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 74
Val Trp Ser Leu Gly
 1           5

<210> 75
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
      peptide

<400> 75
Asn His Pro Trp
 1

<210> 76
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:5'-end
      32P-labeled oligonucleotide primer

<400> 76
cactgactgt atg

<210> 77
<211> 30
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Combined DNA/RNA
      Molecule:oligonucleotide template

<220>
<223> Description of Artificial Sequence:oligonucleotide
      template

<400> 77
ctcgtcagca tcttcaucat acagtcagtg

```

13

30

```

<210> 78
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:poly Gly
      flexible linker

<220>
<221> MOD_RES
<222> (6)..(200)
<223> Gly residues from position 6 to 200 may be present
      or absent

<400> 78
Gly Gly
    1           5           10           15

Gly Gly
    20          25          30

Gly Gly
    35          40          45

Gly Gly
    50          55          60

Gly Gly
    65          70          75          80

Gly Gly
    85          90          95

Gly Gly
    100         105         110

Gly Gly
    115         120         125

Gly Gly
    130         135         140

Gly Gly
    145         150         155         160

Gly Gly
    165         170         175

Gly Gly
    180         185         190

Gly Gly Gly Gly Gly Gly Gly
    195         200

```